

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:09:22 ; Search time 10479 Seconds

(without alignments)  
10025.556 Million cell updates/sec

Title: US-09-854-867-6

Perfect score: 2760

Sequence: 1 cagtcgcttcaactgacgctg...aaaawgttggaagacacgctg 2760

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :  
EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	235.2	8.5	666	9	AG050496 Pan trogl
2	233.4	8.5	497	9	CR737523 CR737523
3	224.8	8.1	668	9	CE769346 Ligr-g88-
4	223	8.1	728	9	CC555035 CH240_461
5	223	8.1	861	9	CC476217 CH240_301
6	220.8	8.0	654	9	CE691282 Ligr-g88-
7	218.4	7.9	627	8	AO506853 RPII-11-2
8	215.4	7.8	622	8	B2883743 CH240_189
9	214.8	7.8	715	5	BQ597867 MT-P-K2-a
10	210.4	7.6	728	9	CE114679 Ligr-g88-
11	207.6	7.5	633	9	CE476563 Ligr-g88-
12	197.4	7.2	701	8	B2867261 CH240_288
13	196	7.1	444	2	AM104660 xds5e03.x
14	191.8	6.9	705	9	CC911866 t068p19ba
15	188.4	6.8	558	8	AO424645 CTRB1-E1-
16	188	6.8	651	9	CLJ01716 g882_CH25
17	186.4	6.8	754	9	CE328397 Ligr-g88-
18	185.2	6.7	619	8	AO200902 RPII1-61
19	184.8	6.7	583	9	CE666755 Ligr-g88-
20	177.4	6.4	834	7	CK449411 892979 MA
21	173.4	6.3	748	5	BM984741 UI-CF-ECL
22	172.8	6.3	514	1	AI990936 w824g10.x
23	171	6.2	689	8	AO390570 CTRB1-E1-
24	170.2	6.2	448	8	AO197912 CIT-HSP-2

25	170.2	6.2	486	1	AU674187	AU674187
26	170.2	6.2	708	8	B2610828	B2610828
27	169.8	6.2	594	8	AO433787	AO433787
28	169	6.1	487	1	AA024442	AA024442
29	168	6.1	485	9	CE745730	CE745730
30	167.8	6.1	504	8	AO006291	AO006291
31	167	6.1	680	1	AL559202	AL559202
32	167	6.1	680	3	CR624325	CR624325
33	167	6.1	696	8	CA426386	CA426386
34	167	6.1	713	5	BM788242	BM788242
35	167	6.1	1530	3	CR591289	CR591289
36	166.8	6.0	650	8	B59993	B59993
37	166.6	6.0	851	8	B2600766	B2600766
38	165.6	6.0	624	9	CE679167	CE679167
39	165.6	6.0	1071	1	AL539196	AL539196
40	165.2	6.0	858	5	BX392511	BX392511
41	165	6.0	652	8	B2852014	B2852014
42	163.8	5.9	765	6	CB963879	CB963879
43	161.8	5.9	690	5	BM980045	BM980045
44	161.6	5.9	514	8	AO368387	AO368387
45	160.8	5.8	654	8	B2861747	B2861747
46	160.6	5.8	682	8	AO316771	AO316771
47	160	5.8	636	5	BX651581	BX651581
48	159.6	5.8	457	8	AO887234	AO887234
49	159.6	5.8	651	1	AL559201	AL559201
50	158.2	5.7	962	4	BG430553	BG430553
51	157.6	5.7	756	9	CE287618	CE287618
52	157.4	5.7	754	8	AO420143	AO420143
53	155.8	5.6	705	9	CL366279	CL366279
54	155.6	5.6	440	9	CE643311	CE643311
55	155.6	5.6	677	9	CE720006	CE720006
56	155.2	5.6	468	5	BX097159	BX097159
57	155.2	5.6	571	9	CE746991	CE746991
58	155	5.6	629	4	BG567813	BG567813
59	155	5.6	737	5	BUC26144	BUC26144
60	154.8	5.6	649	9	CE503254	CE503254
61	153.8	5.6	701	9	CE025080	CE025080
62	151.6	5.5	755	9	CE437336	CE437336
63	151.6	5.5	892	9	ECAS76604	ECAS76604
64	148.2	5.4	390	8	AO284904	AO284904
65	148.2	5.4	568	8	AO711935	AO711935
66	148.2	5.4	580	8	AO721219	AO721219
67	148	5.4	551	9	CE783887	CE783887
68	147.8	5.4	476	1	AA001539	AA001539
69	147	5.3	834	9	CC473177	CC473177
70	145.4	5.3	497	1	AI424388	AI424388
71	145.4	5.3	533	9	CE212519	CE212519
72	145.4	5.3	537	9	CT768396	CT768396
73	145.4	5.3	602	9	CE625577	CE625577
74	144.2	5.2	3579	3	AK034794	AK034794
75	143.4	5.2	673	2	BB092826	BB092826
76	142.4	5.2	655	9	CE449511	CE449511
77	142.4	5.2	749	9	CE288650	CE288650
78	142.2	5.2	721	7	CK837711	CK837711
79	142.2	5.2	506	9	CE598948	CE598948
80	141.6	5.1	372	8	AO145326	AO145326
81	141.2	5.1	506	1	AI467915	AI467915
82	140.6	5.1	535	8	CE556591	CE556591
83	140	5.1	535	8	AO403179	AO403179
84	140	5.1	573	1	AI768650	AI768650
85	139.8	5.0	765	9	CR836892	CR836892
86	138.2	5.0	545	6	CR854010	CR854010
87	137.8	5.0	615	5	BO71441	BO71441
88	137.4	5.0	419	8	AO310173	AO310173
89	137	5.0	590	5	BX552227	BX552227
90	135.6	4.9	684	2	BB636408	BB636408
91	135.6	4.9	1090	3	AK041126	AK041126
92	135.2	4.9	463	8	AO083595	AO083595
93	135.2	4.9	699	9	CL350111	CL350111
94	135.2	4.9	830	9	CR130024	CR130024
95	134.2	4.8	793	9	CE58398	CE58398
96	133.2	4.8	757	9	CC925716	CC925716

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 1798.09 Seconds  
(Without alignments)  
9130.760 Million cell updates/sec

Title: US-09-854-867-6  
Perfect score: 2760  
Sequence: 1 cagtgcttcaactgagcggg.....aaaawgttgaagaccatcg 2760

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database:

Published Applications NA:  
1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/prodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
12: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
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15: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
16: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
17: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
18: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
19: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2716.6	98.4	2760	US-09-854-867-6	Sequence 6, Appli
2	516.8	18.7	198285	US-09-880-107-3814	Sequence 318, Ap
3	516.8	18.7	198285	US-10-775-169-338	Sequence 318, Ap
4	440.8	16.0	62647	US-10-322-281-274	Sequence 274, Ap
5	400.8	14.5	3673778	US-10-312-841-2	Sequence 2, Appli
6	371.6	11.6	293625	US-10-719-993-6929	Sequence 1, Appli
7	320	9.5	209484	US-10-087-192-418	Sequence 418, Ap
8	261	9.5	209484	US-10-331-053-4	Sequence 4, Appli
9	261	9.3	194883	US-10-087-192-826	Sequence 826, Ap
10	256	9.1	53323	US-10-741-601-5695	Sequence 5695, Ap
11	251				

12	251	9.1	53323	US-10-741-600-17769	Sequence 17769, A
13	248.6	9.0	78025	US-10-020-141-9	Sequence 9, Appli
14	247	8.9	101685	US-10-723-860-146	Sequence 146, Ap
15	210.4	7.6	147620	US-10-723-860-2768	Sequence 2768, Ap
16	210.2	7.6	72604	US-10-162-497-7	Sequence 7, Appli
17	210.2	7.6	72604	US-10-629-313-7	Sequence 7, Appli
18	207.2	7.5	122814	US-10-741-600-17762	Sequence 17652, A
19	205.2	7.4	3131	US-10-027-632-114343	Sequence 114343, A
20	205.2	7.4	3131	US-10-027-632-114344	Sequence 114344, A
21	205.2	7.4	3131	US-10-027-632-114343	Sequence 114343, A
22	205.2	7.4	3131	US-10-027-632-114344	Sequence 114344, A
23	204.4	7.4	1001	US-10-294-934-24	Sequence 24, Appli
24	197	7.1	125796	US-10-719-993-6804	Sequence 6804, Ap
25	193.4	7.0	15951	US-10-311-455-1654	Sequence 1654, Ap
26	193.4	7.0	15951	US-10-240-485-134	Sequence 134, Ap
27	190	6.9	17491	US-10-240-485-128	Sequence 128, Ap
28	188	6.8	611	US-10-027-632-305785	Sequence 305785, A
29	188	6.8	611	US-10-027-632-305785	Sequence 305785, A
30	188	6.8	611	US-10-027-632-305785	Sequence 305785, A
31	188	6.8	611	US-10-027-632-305785	Sequence 305785, A
32	187.4	6.8	42479	US-10-719-993-6964	Sequence 6964, Ap
33	187.4	6.8	42479	US-10-741-600-17900	Sequence 17900, A
34	187.4	6.8	1980090	US-10-719-993-6815	Sequence 6815, Ap
35	187.4	6.8	1980090	US-10-741-600-17676	Sequence 17676, A
36	185.8	6.7	96592	US-09-997-722-88	Sequence 88, Appli
37	185.2	6.7	15951	US-10-311-455-1653	Sequence 1653, Ap
38	185.2	6.7	15951	US-10-240-485-133	Sequence 133, Ap
39	176.6	6.4	12079	US-09-764-847-1880	Sequence 1880, Ap
40	176.6	6.4	12079	US-10-092-154-1880	Sequence 1880, Ap
41	174.6	6.3	40060	US-10-388-838-68	Sequence 68, Appli
42	173.4	6.3	554	US-10-357-930-5854	Sequence 5854, A
43	169.2	6.1	118931	US-10-087-192-1108	Sequence 1108, Ap
44	165.8	6.0	138837	US-10-332-281-146	Sequence 146, Ap
45	164.6	6.0	197997	US-09-822-246-3	Sequence 3, Appli
46	164.6	6.0	197997	US-10-469-028-3	Sequence 3, Appli
47	162	5.9	599	US-09-878-722-64	Sequence 64, Appli
48	162	5.9	599	US-09-904-456-64	Sequence 64, Appli
49	161.8	5.9	79860	US-10-087-192-112	Sequence 112, Ap
50	161.4	5.8	91000	US-10-002-491-10	Sequence 10, Appli
51	160	5.8	601	US-09-796-692-8236	Sequence 8236, Ap
52	160	5.8	601	US-10-040-862-8236	Sequence 8236, Ap
53	160	5.8	601	US-10-057-475B-8236	Sequence 8236, Ap
54	160	5.8	601	US-10-154-884B-8236	Sequence 8236, Ap
55	160	5.8	601	US-10-764-324-8236	Sequence 8236, Ap
56	159.6	5.8	9179	US-09-955-866-16	Sequence 16, Appli
57	159.2	5.8	17491	US-10-240-485-127	Sequence 127, Ap
58	158.6	5.7	629	US-10-027-632-207610	Sequence 207610, A
59	158.6	5.7	629	US-10-027-632-207611	Sequence 207611, A
60	158.6	5.7	629	US-10-027-632-207612	Sequence 207612, A
61	158.6	5.7	629	US-10-027-632-207610	Sequence 207610, A
62	158.6	5.7	629	US-10-027-632-207611	Sequence 207611, A
63	158.6	5.7	629	US-10-027-632-207612	Sequence 207612, A
64	158.6	5.7	79684	US-10-034-650-40	Sequence 40, Appli
65	155	5.6	84539	US-09-962-436-36	Sequence 36, Appli
66	153.6	5.6	227931	US-10-085-117-274	Sequence 274, Ap
67	153.2	5.6	119472	US-10-741-600-17865	Sequence 17865, A
68	153.2	5.6	255015	US-10-741-600-17611	Sequence 17611, A
69	152	5.5	120239	US-10-322-281-271	Sequence 271, Ap
70	148.4	5.4	676	US-10-027-632-196564	Sequence 196564, A
71	148.4	5.4	676	US-10-027-632-196565	Sequence 196565, A
72	148.4	5.4	676	US-10-027-632-196564	Sequence 196564, A
73	148.4	5.4	676	US-10-027-632-196565	Sequence 196565, A
74	148	5.4	98850	US-10-719-993-6798	Sequence 6798, Ap
75	147.8	5.4	476	US-09-954-456-1725	Sequence 1725, Ap
76	147.8	5.4	96594	US-09-997-722-154	Sequence 154, Ap
77	144.8	5.2	575	US-10-027-632-61037	Sequence 61037, A
78	144.8	5.2	575	US-10-027-632-61037	Sequence 61037, A
79	144.8	5.2	575	US-10-027-632-61037	Sequence 61037, A
80	144.8	5.2	575	US-10-027-632-61038	Sequence 61038, A
81	144.8	5.2	577	US-10-027-632-109727	Sequence 109727, A
82	144.8	5.2	577	US-10-027-632-109728	Sequence 109728, A
83	144.8	5.2	577	US-10-027-632-109727	Sequence 109727, A
84	144.8	5.2	577	US-10-027-632-109728	Sequence 109728, A

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 502.914 Seconds  
(without alignments)  
8979.909 Million cell updates/sec

Title: US-09-854-867-6  
Perfect score: 2760  
Sequence: 1 cagtgcttcacacacg999.....aaaawgttcgaagaccacg 2760

Scoring table: IDENTITY\_NIC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents NA :  
1: /cgn2\_6/prodata/1/ina/5A\_COMB\_seq.\*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB\_seq.\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB\_seq.\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB\_seq.\*  
5: /cgn2\_6/prodata/1/ina/PCUTS\_COMB\_seq.\*  
6: /cgn2\_6/prodata/1/ina/backfillseq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2716.6	98.4	2760	US-09-573-080A-6	Sequence 6, Appl
2	340.2	12.3	312474	US-09-949-016-17434	Sequence 17434, A
3	262.6	9.5	108169	US-09-949-016-12898	Sequence 12898, A
4	262.6	9.5	108169	US-09-949-016-15907	Sequence 15907, A
5	256	9.3	178884	US-09-949-016-12733	Sequence 12733, A
6	256	9.3	178884	US-09-949-016-13039	Sequence 13039, A
7	248.6	9.0	45323	US-09-949-016-16142	Sequence 16142, A
8	243.4	8.8	89689	US-09-949-016-13089	Sequence 13089, A
9	215.4	7.8	231129	US-09-949-016-16110	Sequence 16110, A
10	215.4	7.8	266293	US-09-949-016-11934	Sequence 11934, A
11	210.2	7.6	72604	US-09-268-992-7	Sequence 7, Appl
12	210.2	7.6	72604	US-09-657-474-7	Sequence 7, Appl
13	205.4	7.4	17730	US-09-949-016-12123	Sequence 12123, A
14	205.4	7.4	17730	US-09-949-016-13472	Sequence 13472, A
15	204.4	7.4	1001	US-09-671-317-24	Sequence 24, Appl
16	201.8	7.3	601	US-09-949-016-148420	Sequence 148420, A
17	195.4	7.1	40951	US-09-949-016-158459	Sequence 158459, A
18	181.8	6.6	83938	US-09-949-016-16068	Sequence 16068, A
19	177.8	6.4	149543	US-09-949-016-15847	Sequence 15847, A
20	177.8	6.4	80632	US-09-949-016-12951	Sequence 12951, A
21	174.6	6.3	254405	US-09-949-016-15881	Sequence 15881, A
22	172.6	6.3	26134	US-09-949-016-15881	Sequence 15881, A
23	170.6	6.2	253375	US-09-949-016-15849	Sequence 15849, A
24	169.6	6.1	192302	US-09-949-016-15770	Sequence 15770, A
25	167.6	6.1	72128	US-09-949-016-16018	Sequence 16018, A
26	165.2	6.0	145812	US-09-949-016-15698	Sequence 15698, A
27	161.4	5.8	94019	US-09-949-016-13203	Sequence 13203, A

28	161	5.8	601	US-09-949-016-157716	Sequence 157716, A
29	158.6	5.7	63544	US-09-949-016-14025	Sequence 14025, A
30	156.6	5.7	187580	US-09-949-016-12266	Sequence 12266, A
31	156.2	5.7	601	US-09-949-016-52641	Sequence 52641, A
32	155.4	5.6	87216	US-09-949-016-15891	Sequence 15891, A
33	155.2	5.6	601	US-09-949-016-52642	Sequence 52642, A
34	153.4	5.6	294836	US-09-949-016-15974	Sequence 15974, A
35	152.6	5.5	114139	US-09-949-016-15536	Sequence 15536, A
36	149.4	5.4	601	US-09-949-016-159960	Sequence 159960, A
37	148.8	5.4	601	US-09-949-016-112491	Sequence 112491, A
38	147.8	5.4	187595	US-09-949-016-15546	Sequence 15546, A
39	147.6	5.4	601	US-09-949-016-169959	Sequence 169959, A
40	147.6	5.3	450395	US-09-949-016-15473	Sequence 15473, A
41	147.2	5.3	601	US-09-949-016-12450	Sequence 12450, A
42	146.6	5.3	99500	US-09-798-096-10	Sequence 10, Appl
43	146	5.3	601	US-09-949-016-41579	Sequence 41579, A
44	145.6	5.3	601	US-09-949-016-12798	Sequence 12798, A
45	144.8	5.2	45183	US-09-949-016-12798	Sequence 12798, A
46	144.8	5.2	96932	US-09-949-016-17061	Sequence 17061, A
47	144.8	5.2	194537	US-09-949-016-12928	Sequence 12928, A
48	144.8	5.2	201529	US-09-949-016-12740	Sequence 12740, A
49	144.2	5.2	11494	US-09-949-016-13347	Sequence 13347, A
50	143.6	5.2	147321	US-09-949-016-15450	Sequence 15450, A
51	142.8	5.2	1001	US-09-671-317-25	Sequence 25, Appl
52	134.2	4.9	99916	US-09-816-095-3	Sequence 3, Appl
53	132.2	4.8	601	US-09-949-016-157715	Sequence 157715, A
54	131.6	4.8	17607	US-09-949-016-15968	Sequence 15968, A
55	130.6	4.7	19062	US-09-949-016-14877	Sequence 14877, A
56	130.6	4.7	205044	US-09-949-016-15851	Sequence 15851, A
57	130.6	4.7	205044	US-09-949-016-15851	Sequence 15851, A
58	130.6	4.7	205044	US-09-949-016-15853	Sequence 15853, A
59	130.6	4.7	223471	US-09-949-016-12387	Sequence 12387, A
60	130.6	4.7	223471	US-09-949-016-12725	Sequence 12725, A
61	130.6	4.7	223471	US-09-949-016-154471	Sequence 154471, A
62	129.8	4.7	83708	US-09-949-016-17207	Sequence 17207, A
63	129.6	4.7	260247	US-09-949-016-13358	Sequence 13358, A
64	128.8	4.7	601	US-09-949-016-153658	Sequence 153658, A
65	128.8	4.7	24847	US-09-949-016-16086	Sequence 16086, A
66	127.4	4.6	601	US-09-949-016-170386	Sequence 170386, A
67	127.2	4.6	94830	US-09-949-016-12414	Sequence 12414, A
68	127.2	4.6	94830	US-09-949-016-16336	Sequence 16336, A
69	126.8	4.6	601	US-09-949-016-164030	Sequence 164030, A
70	126.2	4.6	601	US-09-949-016-170385	Sequence 170385, A
71	126.2	4.6	27270	US-09-949-016-13822	Sequence 13822, A
72	125.8	4.6	601	US-09-949-016-120367	Sequence 120367, A
73	125.8	4.6	89843	US-09-949-016-13556	Sequence 13556, A
74	124.6	4.5	89843	US-09-949-016-16566	Sequence 16566, A
75	123.4	4.5	601	US-09-949-016-14547	Sequence 14547, A
76	123.4	4.4	818128	US-09-949-016-14547	Sequence 14547, A
77	122.4	4.4	818128	US-09-949-016-14548	Sequence 14548, A
78	122.4	4.4	818128	US-09-949-016-14549	Sequence 14549, A
79	122.4	4.4	818128	US-09-949-016-14550	Sequence 14550, A
80	122.4	4.4	818128	US-09-949-016-14551	Sequence 14551, A
81	122.4	4.4	818128	US-09-949-016-14552	Sequence 14552, A
82	122.4	4.4	818128	US-09-949-016-14553	Sequence 14553, A
83	122.4	4.4	818128	US-09-949-016-14554	Sequence 14554, A
84	122.4	4.4	818128	US-09-949-016-14555	Sequence 14555, A
85	122.4	4.4	818128	US-09-949-016-14556	Sequence 14556, A
86	122.4	4.4	818128	US-09-949-016-14557	Sequence 14557, A
87	122.4	4.4	818128	US-09-949-016-14558	Sequence 14558, A
88	122.4	4.4	818128	US-09-949-016-14559	Sequence 14559, A
89	122.4	4.4	818128	US-09-949-016-14560	Sequence 14560, A
90	122.4	4.4	818128	US-09-949-016-14561	Sequence 14561, A
91	122.4	4.4	818128	US-09-949-016-14562	Sequence 14562, A
92	122.4	4.4	818128	US-09-949-016-14563	Sequence 14563, A
93	122.4	4.4	818128	US-09-949-016-14564	Sequence 14564, A
94	122.4	4.4	818128	US-09-949-016-14565	Sequence 14565, A
95	122.4	4.4	818128	US-09-949-016-14566	Sequence 14566, A
96	122.4	4.4	818128	US-09-949-016-14567	Sequence 14567, A
97	122.2	4.4	246230	US-09-949-016-17019	Sequence 17019, A
98	122.2	4.4	246230	US-09-949-016-17020	Sequence 17020, A
99	122.2	4.4	246230	US-09-949-016-17021	Sequence 17021, A
100	122.2	4.4	246230	US-09-949-016-17022	Sequence 17022, A

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:44:41 ; Search time 1656.86 seconds  
(without alignments)  
9861.108 Million cell updates/sec

Title: US-09-854-867-6  
Perfect score: 2760  
Sequence: 1 cagtgcttcaactgagcggg.....aaaawgttgaagaccactg 2760

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneeqn1980s:\*  
2: geneeqn1980s:\*  
3: geneeqn2000s:\*  
4: geneeqn2001as:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002as:\*  
7: geneeqn2002bs:\*  
8: geneeqn2003as:\*  
9: geneeqn2003bs:\*  
10: geneeqn2003cs:\*  
11: geneeqn2003ds:\*  
12: geneeqn2004as:\*  
13: geneeqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2716.6	98.4	2760	7	ADG30973 Human gen
2	516.8	18.7	198285	6	ABK84699 Human CDN
3	516.8	18.7	198285	6	ABN97319 Gene #381
4	516.8	18.7	198285	13	ADRS2987 Drug ther
5	440.8	16.0	62647	13	ABD33246 Human can
6	261	9.5	209484	11	ACN44126 Human gen
7	256	9.3	194883	11	ACN44338 Human gen
8	248.6	9.0	78025	8	ABO77404 Human SEL
9	247	8.9	101685	12	ADQ17329 Osteocarc
10	210.4	7.6	147620	10	ADL13739 Human can
11	210.4	7.6	147620	12	ADQ17329 Osteocarc
12	210.2	7.6	72604	2	AAZ10752 Genomic s
13	210.2	7.6	72604	6	ABK43231 Human HKN
14	204.4	7.4	1001	3	AAH51133 Human MGS
15	197.6	7.2	2024	4	AAK90504 Human dig
16	195.2	7.1	88892	12	ADQ97695 Human can
17	193.4	7.0	15951	6	ABL34581 Human met
18	193.4	7.0	15951	6	ABL34581 Human met
19	193.4	7.0	15951	6	ABL70374 Chemical
20	193.4	7.0	15951	7	ADG99842 Complemen

21	190	6.9	17491	6	ABL34575 Human met
22	190	6.9	17491	7	ADG99836 Complemen
23	189.8	6.9	2026	4	AAK90503 Human dig
24	185.8	6.7	96591	10	ADG85301 Mouse SOS
25	185.8	6.7	96592	9	ADG85301 Mouse SOS
26	185.8	6.7	96592	10	ADG85301 Mouse SOS
27	185.8	6.7	96592	12	ADG85301 Mouse SOS
28	185.2	6.7	15951	6	ABL34580 Human met
29	185.2	6.7	15951	6	ABL34580 Human met
30	185.2	6.7	15951	6	ABL70373 Chemical
31	185.2	6.7	15951	7	ADG99841 Bisulphit
32	182.6	6.6	79603	13	ABD33268 7
33	176.6	6.4	12079	4	ABK42293 Genomic s
34	176.6	6.4	12079	4	ABK42293 Genomic s
35	174.6	6.3	100660	13	ABD33272 3
36	173.4	6.3	554	5	ABV58515 Human pro
37	169.2	6.1	118931	11	ACN44586 Human gen
38	167	6.1	147724	6	ABK83566 Human CDN
39	165.8	6.0	138837	13	ABD33163 Human can
40	165.6	6.0	46366	4	AAK82098 Human imm
41	164.6	6.0	197997	10	AAI54074 Human tra
42	162	5.9	599	6	ABK27627 Human col
43	161.8	5.9	79860	11	ACN44122 Human gen
44	161.4	5.8	91000	9	AAI61326 Human far
45	159.6	5.8	9179	6	ADG36971 Human B7-
46	159.2	5.8	17491	6	ABL34574 Human met
47	159.2	5.8	17491	7	ADG99835 Bisulphit
48	158.6	5.7	79690	11	ADL27152 Human gen
49	158.6	5.7	79684	9	ADG03074 Human hCG
50	158.6	5.7	79684	9	ADG66358 Human hCG
51	158.6	5.7	79684	10	ADG72812 Human hCG
52	157.4	5.7	2020	4	AAK90502 Human dig
53	155	5.6	1359	6	AAI47527 Human DNA
54	155	5.6	84539	6	ABL64158 Human DNA
55	155	5.6	84539	10	ADL13479 Human chr
56	152.6	5.5	68940	2	AAK88502 Human dig
57	152	5.5	983	4	AAK88502 Human dig
58	152	5.5	120239	13	ABD33244 Murine ca
59	147.8	5.4	476	6	ABL66415 Lung can
60	146.6	5.3	96593	10	ADG85367 Human BLM
61	146.6	5.3	96594	9	ADG02888 Human BLM
62	146.6	5.3	96594	10	ADG72626 Human BLM
63	146.6	5.3	96594	12	ADG74483 Human car
64	146.6	5.3	99500	6	AAI41740 Human REC
65	143.6	5.2	163321	11	ACN43898 Human gen
66	142.8	5.2	1001	3	AAH51134 Human MGS
67	136.8	5.0	4576	8	ABK63703 Human CDN
68	136.8	5.0	56181	12	ADG97207 Human can
69	136.8	5.0	56181	12	ADG97207 Human can
70	136.4	4.9	157875	6	ABG76673 Human CAD
71	136.4	4.9	160820	8	ABG76673 Human CAD
72	134.2	4.9	99916	6	ADL03931 Human enz
73	134.2	4.9	116297	12	ADQ97587 Human can
74	131.4	4.8	58952	11	ACN44974 Human gen
75	130	4.7	217409	11	ACN44150 Human gen
76	129.6	4.7	86624	9	AAI62889 Human alp
77	129.6	4.7	277616	13	ABD33602 Human can
78	127.8	4.6	23989	4	AAK72555 Human imm
79	127.8	4.6	27860	4	AAK69779 Human imm
80	127.8	4.6	27960	5	AAK73320 Human imm
81	127.8	4.6	27960	5	AAK73320 Human imm
82	126.6	4.6	96593	9	ADG02885 Mouse BLM
83	126.6	4.6	96593	10	ADG72623 Mouse BLM
84	126.6	4.6	96593	12	ADG72623 Mouse BLM
85	126.6	4.6	96594	10	ADG85364 Human pap
86	120.4	4.4	467	4	AAH88332 CNS disor
87	119.8	4.3	4883	3	AAK79410 Human imm
88	119.8	4.3	325	6	AAH96517 Gene #301
89	119	4.3	301	3	AAI5590 Human sec
90	118.8	4.3	177851	8	AAI57272 AA438B23-
91	118.2	4.3	457	9	AAH15429 Human adu
92	116.6	4.2	4129	3	AAH15429 Human adu
93	116.6	4.2	4129	8	AAH15429 Human sec

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 12660.7 Seconds  
(without alignments)  
10563.118 Million cell updates/sec

Title: US-09-854-867-6

Perfect score: 2760  
Sequence: 1 cagtggtcttcaactcgtggtg.....aaaawgttgaagaccactg 2760

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

Genbank1:\*  
1: gb\_ba:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vt:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	546.8	19.8	95556	CR752645 Human DNA
2	546.8	19.8	95788	AL935042 Human DNA
3	546.8	19.8	98309	AL671924 Homo sapi
4	546.8	19.8	110856	EX927138 Human DNA
5	546.8	19.8	114576	EX088556 Human DNA
6	546.8	19.8	118408	CR759798 Human DNA
7	546.8	19.8	126988	CR659918 Human DNA
8	546.8	19.8	166801	AL671681 Human DNA
9	546.8	19.8	175571	AC022567 Homo sapi
10	546.8	19.8	217306	CR354548 Mus muscu
11	516.8	18.7	198285	CQ861705 Sequence
12	516.8	18.7	198285	AX411170 Sequence
13	516.8	18.7	198285	HSEVMHC
14	486.8	17.6	177726	AC148671 Macaca mu
15	485.2	17.6	176807	AC002384 Homo sapi
16	442.2	16.1	69248	AC002384 Homo sapi
17	442.8	16.0	44670	CR762464 Homo sapi
18	440.8	16.0	184302	AL162393 Human DNA
19	439.2	15.9	143388	AC146122 Pan trogl

20	412.2	14.9	188061	AC007373
21	410.4	14.9	163312	AC007955 Homo sapi
22	410.4	14.9	177172	CNS0000G
23	400.8	14.5	349980	AX344554 Sequence
24	400	14.5	154485	AC068934 Homo sapi
25	400	14.5	164084	AP006264 Homo sapi
26	400	14.5	172665	AC140019 Homo sapi
27	400	14.5	197065	AC090686 Homo sapi
28	371.6	13.5	349980	AX344550 Sequence
29	369.2	13.4	158688	AF238380 Homo sapi
30	369.2	13.4	171901	AC027240 Homo sapi
31	369.2	13.4	176364	AC126322 Homo sapi
32	368.8	13.4	159629	AC098616 Homo sapi
33	360.6	13.1	195568	AC092503 Homo sapi
34	360	13.0	133445	AC073440 Homo sapi
35	360	13.0	170270	AP001548 Homo sapi
36	360	13.0	174645	AC091111 Homo sapi
37	360	13.0	175850	AP001399 Homo sapi
38	360	13.0	194487	AP002896 Homo sapi
39	360	13.0	204340	AC091103 Homo sapi
40	358.4	13.0	161674	AP001493 Homo sapi
41	358.4	13.0	170413	AC090405 Homo sapi
42	358.4	13.0	186150	AP001544 Homo sapi
43	356.2	12.9	166715	HS30801
44	354.6	12.8	142346	AC110992 Homo sapi
45	354.6	12.8	146460	AC024387 Homo sapi
46	354.2	12.8	181745	AC008179 Homo sapi
47	354.2	12.8	79000	AP006295 Homo sapi
48	354.2	12.8	180973	AC022316 Homo sapi
49	352.6	12.8	169248	AC145907 Homo sapi
50	340.2	12.3	113028	HS68D15
51	333.4	12.1	138028	AC103743 Homo sapi
52	333.4	12.1	164879	AC022684 Homo sapi
53	333.4	12.1	217659	AC116157 Homo sapi
54	331.6	12.0	43347	AL138734 Homo sapi
55	330	12.0	159070	AL354939 Homo sapi
56	321.6	11.7	67446	AL354939 Homo sapi
57	320.6	11.6	21533	HS352811 Homo sapi
58	320	11.6	169986	AL355589 Homo sapi
59	320	11.6	183104	AL355601 Homo sapi
60	320	11.6	208026	AP006292 Homo sapi
61	318.8	11.6	129894	AC108181 Felis cat
62	318.8	11.6	138649	AC146892 Dasypus n
63	312	11.3	209521	AC021649 Homo sapi
64	311.6	11.3	127360	AC099409 Felis cat
65	311.6	11.3	135855	AC098701 Felis cat
66	310.8	11.3	170543	AC021012 Homo sapi
67	310.8	11.3	170544	CNS050TC
68	307.8	11.2	149408	AC146272 Homo sapi
69	307.8	11.2	171165	AC142352 Pan trogl
70	306.8	11.1	179844	AC009255 Homo sapi
71	306.4	11.1	159620	AC087069 Homo sapi
72	306.4	11.1	167942	AC021654 Homo sapi
73	303.6	11.0	161874	AC114482 Homo sapi
74	303.2	11.0	131303	AL355974 Human DNA
75	301.8	10.9	141833	AL442063 Human DNA
76	301.8	10.9	165904	AL158148 Homo sapi
77	299.2	10.8	81487	HS0770C23
78	298.6	10.8	164908	AC012439 Homo sapi
79	298.6	10.8	194374	AC018676 Homo sapi
80	297	10.8	91377	AC018667 Homo sapi
81	297	10.8	93497	AC068009 Homo sapi
82	297	10.8	256381	AC03610 Homo sapi
83	295.4	10.7	94568	AC114973 Homo sapi
84	295.4	10.7	157751	AC016644 Homo sapi
85	295.4	10.7	165287	AC034165 Homo sapi
86	292.8	10.6	143993	AC093607 Homo sapi
87	292.8	10.6	174274	AC044905 Homo sapi
88	291.6	10.6	175919	AC040918 Homo sapi
89	290.6	10.5	100167	HS131916 Human DNA
90	288.8	10.5	181013	AC148288 Rhinolph
91	287.2	10.4	139617	AC146889 Bos tauru
92	286.6	10.4	24206	AC128658 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 1784.41 Seconds  
(without alignments)  
9130.760 Million cell updates/sec

Title: US-09-854-867-5  
Perfect score: 2739  
Sequence: 1 cagcggttcacgaagtcg.....aaaagttgagacgcgtg 2739

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications NA.\*

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2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTOS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10F\_NEW\_PUB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2733.2	99.8	2739	10	US-09-854-867-5
2	1304	47.6	1450	10	US-09-854-867-5
3	820.2	29.9	209822	19	US-10-741-600-17560
4	675	24.6	198285	9	US-09-880-107-3814
5	597.4	21.8	3451	13	US-10-775-169-338
6	597.4	21.8	3451	13	US-10-027-632-115204
7	593.6	21.7	31724	17	US-10-027-632-115204
8	593.6	21.7	31724	17	US-10-087-192-766
9	590	21.5	75395	17	US-10-331-053-76
10	590	21.5	75395	17	US-10-274-154-3
11	590	21.5	75395	18	US-10-760-407-3

12	566	20.7	337022	18	US-10-322-696-52	Sequence 52, Appl
13	544.6	19.9	58320	18	US-10-322-281-88	Sequence 88, Appl
14	541.2	19.8	160771	18	US-10-450-826-86	Sequence 86, Appl
15	539.8	19.7	209484	13	US-10-087-192-418	Sequence 418, Appl
16	539.8	19.7	209484	18	US-10-331-053-4	Sequence 4, Appl
17	529.6	19.3	80815	18	US-10-322-281-486	Sequence 486, Appl
18	529.6	19.3	3352	17	US-10-027-632-115478	Sequence 115478, Appl
19	529.6	19.3	3352	17	US-10-027-632-115478	Sequence 115478, Appl
20	523.2	19.1	209802	19	US-10-085-117-286	Sequence 286, Appl
21	520.8	19.0	119472	17	US-10-741-600-17865	Sequence 17865, Appl
22	504.4	18.4	187844	18	US-10-719-993-6883	Sequence 6883, Appl
23	503.6	18.4	25950	9	US-09-764-891-10135	Sequence 10135, Appl
24	503.6	18.4	25950	14	US-10-125-540-597	Sequence 597, Appl
25	503.6	18.4	196686	13	US-10-087-192-484	Sequence 484, Appl
26	503.2	18.4	2756	10	US-09-814-353-20143	Sequence 20143, Appl
27	503.2	18.4	2756	14	US-10-198-846-9729	Sequence 9729, Appl
28	495.4	18.1	32249	13	US-09-764-891-7477	Sequence 7477, Appl
29	491.6	17.9	228139	13	US-10-087-192-232	Sequence 232, Appl
30	479.8	17.5	414295	18	US-10-719-993-6876	Sequence 6876, Appl
31	479	17.5	85506	17	US-10-085-117-220	Sequence 220, Appl
32	464	16.9	260209	15	US-10-025-966A-23	Sequence 23, Appl
33	464	16.9	260209	15	US-10-322-281-252	Sequence 252, Appl
34	456.2	16.7	161531	18	US-10-322-281-252	Sequence 252, Appl
35	449	16.4	62520	18	US-10-266-103-338	Sequence 338, Appl
36	445.6	16.3	15643	9	US-09-764-870-638	Sequence 638, Appl
37	445.6	16.3	15643	14	US-10-125-540-638	Sequence 638, Appl
38	434.4	15.9	66312	13	US-10-087-192-1054	Sequence 1054, Appl
39	424.4	15.5	3179	13	US-10-027-632-113290	Sequence 113290, Appl
40	424.4	15.5	3179	13	US-10-027-632-113291	Sequence 113291, Appl
41	424.4	15.5	3179	17	US-10-027-632-113290	Sequence 113290, Appl
42	424.4	15.5	3179	17	US-10-027-632-113291	Sequence 113291, Appl
43	417	15.2	350570	18	US-10-417-375-146	Sequence 146, Appl
44	409.8	15.0	98439	19	US-10-741-600-17724	Sequence 17724, Appl
45	409.8	15.0	112604	18	US-10-723-860-970	Sequence 970, Appl
46	407	14.9	3673778	16	US-10-312-841-1	Sequence 1, Appl
47	406.6	14.8	1477	10	US-09-892-877-26	Sequence 26, Appl
48	406.6	14.8	1477	10	US-09-948-783-27	Sequence 27, Appl
49	406.2	14.8	197526	18	US-10-322-281-498	Sequence 498, Appl
50	405.6	14.8	142318	13	US-10-087-192-1504	Sequence 1504, Appl
51	405.2	14.8	177380	19	US-10-484-577-683	Sequence 683, Appl
52	396.2	14.5	161334	13	US-10-087-192-730	Sequence 730, Appl
53	394.2	14.4	3673778	16	US-10-312-841-2	Sequence 2, Appl
54	389.4	14.2	83712	18	US-10-741-601-5705	Sequence 5705, Appl
55	389.4	14.2	83712	19	US-10-052-482-82	Sequence 17805, Appl
56	384.6	14.0	87878	17	US-10-322-281-54	Sequence 54, Appl
57	382.8	13.7	21045	9	US-09-764-864-1695	Sequence 1695, Appl
58	374.8	13.6	67810	13	US-10-087-192-1738	Sequence 1738, Appl
59	373.4	13.6	149612	13	US-10-087-192-1960	Sequence 1960, Appl
60	371.6	13.6	4319	10	US-09-764-891-8382	Sequence 8382, Appl
61	371.6	13.6	247682	17	US-10-235-192A-28	Sequence 28, Appl
62	370.8	13.5	255011	19	US-10-741-600-17611	Sequence 17611, Appl
63	369.8	13.5	32174	9	US-09-908-711-158	Sequence 158, Appl
64	369.8	13.5	32174	9	US-09-764-860-1134	Sequence 1134, Appl
65	369.8	13.5	32174	9	US-09-764-877-2645	Sequence 2645, Appl
66	369.8	13.5	32174	9	US-09-860-670-232	Sequence 232, Appl
67	369.8	13.5	32174	9	US-09-764-891-10135	Sequence 10135, Appl
68	369.8	13.5	32174	10	US-09-764-891-10135	Sequence 10135, Appl
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72	369.8	13.5	32174	10	US-09-764-891-10135	Sequence 10135, Appl
73	369.8	13.5	32174	14	US-10-091-548-90	Sequence 90, Appl
74	369.8	13.5	32174	14	US-10-074-099-11334	Sequence 11334, Appl
75	369.8	13.5	32174	17	US-10-074-099-11334	Sequence 11334, Appl
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78	369.8	13.5	32174	17	US-10-074-099-11334	Sequence 11334, Appl
79	369.8	13.5	32174	17	US-10-074-099-11334	Sequence 11334, Appl
80	369.8	13.5	32174	17	US-10-074-099-11334	Sequence 11334, Appl
81	369.8	13.5	32174	17	US-10-074-099-11334	Sequence 11334, Appl
82	369.8	13.5	32174	17	US-10-074-099-11334	Sequence 11334, Appl
83	369.8	13.5	32174	17	US-10-074-099-11334	Sequence 11334, Appl
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OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 499.088 Seconds  
(without alignments)  
8979.909 Million cell updates/sec

Title: US-09-854-867-5

Perfect score: 2739  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues.

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents NA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2733.2	99.8	2739	4 US-09-573-080A-5	Sequence 5, Appli
2	1304	47.6	1450	4 US-09-573-080A-418	Sequence 418, App
3	901.2	32.9	247259	4 US-09-949-016-17530	Sequence 17530, A
4	820.2	29.9	197131	4 US-09-949-016-12675	Sequence 12675, A
5	820.2	29.9	197131	4 US-09-949-016-17170	Sequence 17170, A
6	629.8	23.0	235064	4 US-09-949-016-15330	Sequence 15330, A
7	597.4	21.8	374159	4 US-09-949-016-15868	Sequence 15868, A
8	590	21.5	75395	4 US-09-984-890-3	Sequence 3, Appli
9	590	21.5	75395	4 US-10-274-194-3	Sequence 3, Appli
10	578.4	21.1	123863	4 US-09-949-016-14202	Sequence 14202, A
11	567.6	20.7	133719	4 US-09-949-016-15092	Sequence 15092, A
12	563.8	19.9	374159	4 US-09-949-016-15868	Sequence 15868, A
13	542.6	19.8	317365	4 US-09-949-016-16001	Sequence 16001, A
14	540.6	19.4	82000	4 US-09-949-016-15595	Sequence 15595, A
15	531.8	19.4	82000	4 US-09-949-016-15595	Sequence 15595, A
16	520.2	19.0	222691	4 US-09-949-016-15842	Sequence 15842, A
17	520.2	19.0	222691	4 US-09-949-016-15842	Sequence 15842, A
18	510.8	18.6	109250	4 US-09-949-016-12530	Sequence 12530, A
19	510.8	18.6	109250	4 US-09-949-016-12530	Sequence 12530, A
20	491.6	17.9	212139	4 US-09-949-016-16065	Sequence 16065, A
21	488.2	17.8	117391	4 US-09-949-016-13945	Sequence 13945, A
22	477.4	17.4	89892	4 US-09-949-016-13667	Sequence 13667, A
23	475.2	17.3	101894	4 US-09-949-016-12005	Sequence 12005, A
24	475.2	17.3	101894	4 US-09-949-016-14450	Sequence 14450, A
25	472.8	17.3	77994	4 US-09-949-016-12517	Sequence 12517, A
26	472.8	17.3	77994	4 US-09-949-016-16021	Sequence 16021, A
27	467.6	17.1	173787	4 US-09-949-016-12542	Sequence 12542, A

28	467.6	17.1	173791	4 US-09-949-016-17302	Sequence 17302, A
29	456.4	16.7	36338	4 US-09-949-016-13484	Sequence 13484, A
30	452	16.5	55606	4 US-09-949-016-15605	Sequence 15605, A
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33	433	15.8	129127	4 US-09-949-016-13481	Sequence 13481, A
34	432.4	15.8	136917	4 US-09-949-016-16369	Sequence 16369, A
35	431	15.7	13675	4 US-09-949-016-11746	Sequence 11746, A
36	428.1	15.6	103447	4 US-09-949-016-15320	Sequence 15320, A
37	421.6	15.4	67755	4 US-09-949-016-12288	Sequence 12288, A
38	419.4	15.3	76165	4 US-09-949-016-14005	Sequence 14005, A
39	419.4	15.3	76165	4 US-09-949-016-14005	Sequence 14005, A
40	415	15.2	99304	4 US-09-949-016-15440	Sequence 15440, A
41	414.8	15.1	237241	4 US-09-949-016-15101	Sequence 15101, A
42	413.6	15.1	95561	4 US-09-949-016-12768	Sequence 12768, A
43	413.6	15.1	95561	4 US-09-949-016-13306	Sequence 13306, A
44	413.6	15.1	95561	4 US-09-949-016-13307	Sequence 13307, A
45	413	15.1	53789	4 US-09-949-016-12137	Sequence 12137, A
46	413	15.1	53789	4 US-09-949-016-13955	Sequence 13955, A
47	406.6	14.8	172677	4 US-09-949-016-13444	Sequence 13444, A
48	406.2	14.8	183202	4 US-09-949-016-13614	Sequence 13614, A
49	405.6	14.8	60141	4 US-09-949-016-15874	Sequence 15874, A
50	400.6	14.6	67181	4 US-09-949-016-13102	Sequence 13102, A
51	396.2	14.5	145320	4 US-09-949-016-15858	Sequence 15858, A
52	395.2	14.4	98708	4 US-09-949-016-13392	Sequence 13392, A
53	390.4	14.3	126468	4 US-09-949-016-14418	Sequence 14418, A
54	390.4	14.3	131724	4 US-09-949-016-12893	Sequence 12893, A
55	384.6	14.0	71879	4 US-09-949-016-17465	Sequence 17465, A
56	382	13.9	168394	4 US-09-949-016-13002	Sequence 13002, A
57	378.2	13.8	55387	4 US-09-949-016-12993	Sequence 12993, A
58	375	13.7	101011	4 US-09-949-016-16933	Sequence 16933, A
59	373	13.6	133613	4 US-09-949-016-15824	Sequence 15824, A
60	369	13.5	147382	4 US-09-949-016-14624	Sequence 14624, A
61	359.2	13.1	44096	4 US-09-949-016-15208	Sequence 15208, A
62	359.2	13.1	81585	4 US-09-949-016-15427	Sequence 15427, A
63	356.2	13.0	421118	4 US-09-949-016-16297	Sequence 16297, A
64	354.4	12.9	319608	4 US-09-539-333D-1	Sequence 1, Appli
65	353.2	12.9	319608	4 US-09-679-409-1	Sequence 1, Appli
66	348	12.7	38052	4 US-09-949-016-13825	Sequence 13825, A
67	345.6	12.6	636591	4 US-09-949-016-11808	Sequence 11808, A
68	345.6	12.6	636591	4 US-09-949-016-13388	Sequence 13388, A
69	344.6	12.6	518	4 US-09-573-080A-419	Sequence 419, App
70	342	12.5	239527	4 US-09-949-016-15980	Sequence 15980, A
71	334.8	12.2	153866	4 US-09-949-016-16919	Sequence 16919, A
72	333.6	12.2	670690	4 US-09-949-016-12505	Sequence 12505, A
73	333.6	12.2	670690	4 US-09-949-016-14207	Sequence 14207, A
74	330.6	12.1	40655	4 US-09-949-016-12032	Sequence 12032, A
75	330.6	12.1	40655	4 US-09-949-016-13510	Sequence 13510, A
76	330.2	12.1	16378	4 US-09-949-016-17394	Sequence 17394, A
77	329.8	12.0	145241	4 US-09-949-016-17395	Sequence 17395, A
78	329.8	12.0	145241	4 US-09-949-016-17395	Sequence 17395, A
79	329.2	12.0	47683	4 US-09-949-016-16460	Sequence 16460, A
80	321.6	11.7	3001	4 US-09-539-333D-115	Sequence 115, App
81	321.6	11.7	3001	4 US-09-539-333D-217	Sequence 217, App
82	319.4	11.7	601	4 US-09-949-016-151738	Sequence 151738, A
83	314	11.5	421118	4 US-09-949-016-16937	Sequence 16937, A
84	312.8	11.4	113538	4 US-09-949-016-16329	Sequence 16329, A
85	311.8	11.4	346112	4 US-09-949-016-13165	Sequence 13165, A
86	308.8	11.3	38705	4 US-09-949-016-13883	Sequence 13883, A
87	308.8	11.3	38705	4 US-09-949-016-13884	Sequence 13884, A
88	306	11.2	11424	4 US-09-949-016-17014	Sequence 17014, A
89	305	11.1	84236	4 US-09-949-016-17375	Sequence 17375, A
90	304.4	11.1	360404	4 US-09-949-016-13173	Sequence 13173, A
91	303.8	11.1	70262	4 US-09-949-016-16224	Sequence 16224, A
92	301.6	11.0	70262	4 US-09-949-016-13375	Sequence 13375, A
93	301.6	11.0	70262	4 US-09-949-016-12748	Sequence 12748, A
94	301.4	11.0	81001	3 US-09-750-580-1	Sequence 1, Appli
95	299.6	10.9	283358	4 US-09-949-016-13506	Sequence 13506, A
96	299.2	10.8	126234	4 US-09-949-016-13541	Sequence 13541, A
97	296	10.6	156832	4 US-09-949-016-12976	Sequence 12976, A
98	293.4	10.7	94593	4 US-09-949-016-16324	Sequence 16324, A
99	292	10.7	87205	4 US-09-949-016-13330	Sequence 13330, A
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OM nucleic - nucleic search, using SW model

Run on: March 12, 2005, 01:44:41 ; Search time 1644.25 Seconds  
(without alignments)  
9861.108 Million cell updates/sec

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Perfect score: 2739  
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Scoring table: IDENTITY NUC  
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2733.2	99.8	2739	7	AD830972 Human gen
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3	675	24.6	198285	6	ABK84699 Human gen
4	675	24.6	198285	6	ABN97319 Gene #381
5	675	24.6	198285	13	AD852987 Drug ther
6	629.8	23.0	262090	12	AD852987 Drug ther
7	621.2	22.7	46974	12	AD852987 Drug ther
8	593.6	21.7	31724	11	ACN44358 Human gen
9	590	21.5	75395	8	ABX93648 Human gen
10	590	21.5	75395	12	AD852987 Drug ther
11	590	21.5	75395	12	AD852987 Drug ther
12	586	20.7	337022	12	AD852987 Drug ther
13	550.4	20.1	1613	4	AAK81258 Human gen
14	550.4	20.1	1613	4	AAK81258 Human gen
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17	544.6	19.9	58320	13	ABD33125 Human can
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24	503.6	18.4	196686	11	ACN44170 Human gen
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27	503.2	18.4	2756	11	ACN88579 Human ova
28	503.2	18.4	2842	4	AAH17729 Human CDN
29	495.4	18.1	32249	4	AAH104789 Human rep
30	495.4	18.1	32249	4	AB197684 Human tes
31	491.6	17.9	228139	11	ACN44002 Human gen
32	487	17.8	199878	10	ADL17179 Human gen
33	464	16.9	260209	6	AB856564 Human SUL
34	464	16.9	260209	12	ADN16204 Human sul
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38	445.6	16.3	15643	6	ABO66883 Human DNA
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40	445.6	16.3	15643	10	AD831170 Human DNA
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47	413.8	15.1	4153	4	AAK66121 Human sof
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49	409.8	15.0	112604	12	AD832791-1
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52	406.6	14.8	1477	8	ADA39730 Human sec
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54	406.6	14.8	1477	10	AD831155 Human sec
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56	406.2	14.8	197526	13	ABD33389 Human can
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58	405.8	14.8	50000	3	AAK64460 Human can
59	405.6	14.8	142318	11	ACN44850 Human gen
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65	398.2	14.5	21710	4	AAK42185 Human MDR
66	396.8	14.5	3647	4	AAK85989 Human MDR
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68	396.8	14.5	10117	4	AAK85989 Human MDR
69	396.8	14.5	10117	4	AAK85989 Human MDR
70	396.2	14.5	161334	11	ACN44334 Human gen
71	394	14.4	110000	10	ADG70447 2
72	394	14.4	110000	10	ADG70447 2
73	393.2	14.4	164772	10	ABZ79565-2
74	391	14.3	2604	8	ABZ74188 Human sec
75	391	14.3	2604	8	ABZ74188 Human sec
76	391	14.3	2604	8	ABZ74188 Human sec
77	384.6	14.0	87878	9	ADA02576 Human FXB
78	384.6	14.0	87878	10	AD822314 Human FXB
79	384.6	14.0	87878	10	AD822314 Human FXB
80	383.4	14.0	87878	10	AD822314 Human FXB
81	382.8	14.0	2199	4	AAH17409 Human CDN
82	378.6	13.8	6512	4	AAK65586 Human can
83	378.6	13.8	6512	4	AAK65586 Human can
84	377.8	13.7	21045	8	ABX74070 Human nov
85	374.8	13.7	21045	8	ABX74070 Human nov
86	373.4	13.6	1847	11	ACN45006 Human gen
87	373.4	13.6	1847	11	ACN45006 Human gen
88	373.4	13.6	1847	11	ACN45006 Human gen
89	373.4	13.6	1847	11	ACN45006 Human gen
90	371.6	13.6	4319	12	ADL08109 Human rep
91	371.6	13.6	4319	12	ADL08109 Human rep
92	369.8	13.5	32174	4	AAK63638 Human bre
93	369.8	13.5	32174	4	AAK63638 Human bre



OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 12564.4 Seconds  
(without alignments)  
10563.118 Million cell updates/sec

Title: US-09-854-867-5  
Perfect score: 2739  
Sequence: 1 cagcggttcctcaagtcgtg.....aaaagttcgaacgcgtg 2739

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database: GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pi: \*  
9: gb\_pr: \*  
10: gb\_to: \*  
11: gb\_stc: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	901.2	32.9	201387	9 HSP12	AL133500 Homo sapi
2	890.4	32.5	212103	9 CNS01D4	AL133453 Human chr
3	873.6	31.9	127243	9 AL359545	AL135945 Human DNA
4	873.6	31.9	156799	9 AL359548	AL135948 Homo sapi
5	872	31.8	100839	2 AC002417	AC002417 Homo sapi
6	864.6	31.6	153452	2 AC044895	AC044895 Homo sapi
7	857.4	31.3	201322	9 AC091194	AC091194 Homo sapi
8	839.4	30.6	186102	2 AC015905	AL445990 Human DNA
9	839.4	30.6	186102	2 AC015905	AL445990 Homo sapi
10	820.2	29.8	202397	2 AC074394	AL139185 Human DNA
11	815.4	29.8	202397	2 AC074394	AL139185 Homo sapi
12	787.8	28.8	266941	2 AF224629	AF224629 Homo sapi
13	787.2	28.7	169650	2 AC024629	AC024629 Homo sapi
14	755	27.6	173886	9 HSA17G15	AL009174 Human DNA
15	747	27.3	124321	9 AC096946	AC096946 Homo sapi
16	706.2	25.8	131185	9 AC159343	AL139343 Human DNA
17	689	25.2	183774	9 AL596217	AL596217 Human DNA
18	687.4	25.1	172239	2 AC079307	AC079307 Homo sapi

20	686.6	25.1	186622	2 AC023917	AC023917 Homo sapi
21	678	24.8	95556	9 CR752645	CR752645 Human DNA
22	678	24.8	95788	2 AL935042	AL935042 Homo sapi
23	678	24.8	98309	2 AL671924	AL671924 Homo sapi
24	678	24.8	114576	9 BX088556	BX088556 Human DNA
25	678	24.8	119408	9 CR759798	CR759798 Human DNA
26	678	24.8	126988	9 AL669918	AL669918 Human DNA
27	678	24.8	166803	9 AL671681	AL671681 Human DNA
28	678	24.8	177571	2 AC022567	AC022567 Homo sapi
29	678	24.8	177571	2 CR354548	CR354548 Homo sapi
30	676.4	24.7	110856	2 BX927138	BX927138 Human DNA
31	675	24.6	198285	6 CO861705	CO861705 Sequence
32	675	24.6	198285	6 AX411170	AX411170 Sequence
33	665.8	24.3	91774	9 HSERMHC	X87344 H. sapiens D
34	664.6	24.3	39969	2 BX321867	BX321867 Human DNA
35	664.6	24.3	39969	2 HSB245L19	AL049590 Human DNA
36	662.4	24.1	159969	2 AC093165	AC093165 Homo sapi
37	659.2	24.1	159969	2 AC104791	AC104791 Homo sapi
38	659.2	23.8	189269	2 AP006440	AP006440 Homo sapi
39	650.6	23.8	160966	2 AC148387	AC148387 Rhinolo
40	650.6	23.8	170777	2 AC148444	AC148444 Rhinolo
41	650.6	23.6	157410	2 AC013816	AC013816 Homo sapi
42	646.8	23.6	107166	2 AC080120	AC080120 Homo sapi
43	645.8	23.6	107166	2 AL591885	AL591885 Human DNA
44	645.4	23.6	128312	2 AL591885	AL591885 Human DNA
45	641	23.4	9835	9 HSE98F6	282183 Human DNA
46	640.2	23.2	213084	9 HSG164F24	AL050308 Human DNA
47	635.8	23.2	64394	9 AL928596	AL928596 Human DNA
48	629.8	23.0	151977	2 AC015615	AC015615 Homo sapi
49	629.8	23.0	165747	2 AP002340	AP002340 Homo sapi
50	629.8	23.0	202337	2 AC069055	AC069055 Homo sapi
51	625.8	22.8	50988	9 AC104776	AC104776 Homo sapi
52	624.2	22.8	106576	9 AC012666	AC012666 Homo sapi
53	624.2	22.8	106576	2 AC113393	AC113393 Homo sapi
54	624.2	22.8	109347	2 AL137157	AL137157 Human DNA
55	622.2	22.7	154918	2 HSDJ6788	AL121957 Human DNA
56	622.2	22.7	154918	2 AC022244	AC022244 Homo sapi
57	621.2	22.7	143324	9 AL137881	AL137881 Human DNA
58	619.2	22.6	134060	9 AL358354	AL358354 Human DNA
59	614	22.4	194206	9 AC021863	AC021863 Homo sapi
60	612.8	22.4	155021	9 HS774G10	AL034410 Human DNA
61	612.8	22.4	17357	2 AC025342	AC025342 Homo sapi
62	611.2	22.3	154001	9 AC083904	AC083904 Homo sapi
63	610.6	22.3	130506	9 AC068193	AC068193 Homo sapi
64	610.2	22.3	170059	9 AC068193	AC068193 Homo sapi
65	610.2	22.3	183448	2 AC136949	AC136949 Homo sapi
66	609.6	22.3	135430	2 AC112131	AC112131 Homo sapi
67	609.6	22.3	148517	2 AC011147	AC011147 Homo sapi
68	608.8	22.2	151640	2 AC015816	AC015816 Homo sapi
69	608.8	22.2	151640	2 CNS06C7P	AL139078 Human chr
70	608.6	22.2	119794	9 AC007736	AC007736 Homo sapi
71	608.4	22.2	172476	2 AC067778	AC067778 Homo sapi
72	607	22.2	17967	2 AC026228	AC026228 Homo sapi
73	607	22.2	180480	2 AC025506	AC025506 Homo sapi
74	607	22.2	181750	2 AC009551	AC009551 Homo sapi
75	603	22.0	183547	9 AP003781	AP003781 Homo sapi
76	602.6	22.0	177748	9 AP000929	AP000929 Homo sapi
77	602.6	22.0	197195	9 AP002806	AP002806 Homo sapi
78	601.4	22.0	161871	9 BC018663	BC018663 Homo sapi
79	601.4	22.0	161871	9 AC000057	AC000057 Homo sapi
80	601	21.9	78631	9 AC072029	AC072029 Homo sapi
81	600.2	21.9	151566	2 AC137918	AC137918 Felis cat
82	598.8	21.9	151470	2 AC137918	AC137918 Felis cat
83	598.6	21.8	97083	9 HSDJ45315	AL117343 Human DNA
84	596.8	21.8	44670	2 CR762464	CR762464 Homo sapi
85	596.6	21.8	153152	2 AC104154	AC104154 Pan trogl
86	596.6	21.8	161986	2 AC143302	AC143302 Pan trogl
87	596.6	21.8	161986	2 AC151582	AC151582 Pan trogl
88	596.6	21.8	203249	2 AC151582	AC151582 Pan trogl
89	596.6	21.7	163599	2 AC026041	AC026041 Homo sapi
90	595.6	21.7	163599	2 AC026041	AC026041 Homo sapi
91	595.6	21.7	163599	2 AC026041	AC026041 Homo sapi
92	595.2	21.7	152649	9 AC020651	AC020651 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:09:22 ; Search time 1450.35 Seconds  
(without alignments)  
10025.556 Million cell updates/sec

Title: US-09-854-867-4  
Perfect score: 382  
Sequence: 1 ctgcgaacactactactccag.....ctgcctccacatagatc 382

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
EST:  
1: gb\_ests1:  
2: gb\_ests2:  
3: gb\_hnc:  
4: gb\_ests3:  
5: gb\_ests4:  
6: gb\_ests5:  
7: gb\_ests6:  
8: gb\_gsa1:  
9: gb\_gsa2:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	303.2	79.4	865	AO741580	HS_5567_B
2	291	76.2	495	AO547254	RPCI-11-4
3	288.8	75.6	730	AO898417	HS_3135_B
4	285.8	74.8	528	B88675	RPCI11-2405
5	274.8	71.9	609	AO424030	CITBI-EI-
6	274.8	71.9	655	AO355220	RPCI-11-3
7	274.8	71.9	673	BO631891	1123f06_Y
8	273.2	71.5	542	AO392576	CITBI-EI-
9	273.2	71.5	754	BO633309	UI-H-EI-
10	270	70.7	422	AO052415	RPCI11-51
11	270	70.7	547	AO506522	RPCI-11-2
12	268.6	70.3	565	AO281715	RPCI11-94
13	268.6	70.3	528	AZ520082	RPCI-11-7
14	267.8	70.1	398	AO102208	HS_3035_A
15	266.8	69.8	515	AO118585	HS_3012_A
16	266.8	69.8	565	AZ520040	RPCI-11-7
17	266.8	69.8	595	AO201122	RPCI11-46
18	265.4	69.5	426	B73082	RPCI11-11C1
19	263.2	68.9	378	B84447	RPCI11-2405
20	262	68.6	571	AO505941	RPCI-11-2
21	261.4	68.4	506	AO182059	HS_3228_A
22	261.2	68.4	585	AO528593	RPCI-11-3
23	261	68.3	531	AO361200	HS_5038_B
24	261	68.3	663	CB044935	NISC_gco7

25	260.4	68.2	591	AO485537	RPCI-11-2
26	260.4	68.2	656	AO390453	CITBI-EI-
27	260.4	68.2	699	AO542894	RPCI-11-3
28	260.4	68.2	792	CA313369	UI-CF-FNO
29	259.4	67.9	586	AO345530	RPCI11-11
30	258.8	67.7	484	AO507214	RPCI-11-3
31	258.8	67.7	668	AO375147	RPCI11-14
32	258.4	67.6	687	BM992110	UI-H-DEI-
33	257.6	67.4	492	AO206678	HS_3240_A
34	257.2	67.3	675	BM724054	UI-E-EI-
35	256.4	67.1	642	BF508736	UI-H-BI4-
36	256.4	67.1	843	AO749599	HS_5575_A
37	256	67.0	507	AO413561	RPCI-11-1
38	255.8	66.9	540	AO211081	HS_3234_B
39	255.6	66.9	474	AO376719	RPCI11-16
40	255.6	66.9	493	AO374603	RPCI11-16
41	255.6	66.9	559	AO388505	RPCI11-14
42	255.6	66.9	623	AO540002	RPCI-11-3
43	255.4	66.9	578	AO281841	RPCI11-76
44	255.2	66.8	426	AO014220	RPCI11-23
45	254.8	66.7	512	AO148419	HS_3123_A
46	254.2	66.5	478	AO528812	RPCI-11-3
47	254.2	66.5	736	AO527040	CITBI-EI-
48	254	66.5	540	EX477424	DKF2p686H
49	254	66.5	670	AG171695	Pan t1091
50	254	66.5	673	AG146506	Pan t1091
51	253.8	66.4	702	AW976364	EST388473
52	253.2	66.3	522	BI064298	IL3-UT011
53	252.4	66.1	520	AO508451	RPCI-11-2
54	252.4	66.1	821	AO890988	HS_3081_B
55	251.6	65.9	515	BF735890	QV1-K1002
56	251.6	65.8	495	AO319760	RPCI11-10
57	251.2	65.8	589	AO588595	CITBI-EI-
58	250.8	65.7	476	AO720739	HS_5546_B
59	249.8	65.4	981	AO747450	HS_5537_A
60	249.4	65.3	514	AO369065	HS_5022_B
61	249.4	65.3	515	BF929482	IL2-NT020
62	249.4	65.3	589	AO374395	RPCI11-14
63	249.2	65.2	452	AO265445	CITBI-EI-
64	249.2	65.2	657	AO588714	CITBI-EI-
65	249	65.1	466	AO720853	HS_5546_B
66	248.6	65.1	429	BF841742	RC2-H1108
67	248	64.9	554	BS052085	DKF2p779P
68	247.8	64.9	431	W79549	z476f10.r1
69	247.6	64.8	444	AO635356	RPCI-11-4
70	246.6	64.6	489	AO126203	HS_3035_A
71	246.2	64.5	706	AO423497	CITBI-EI-
72	246.2	64.4	516	AO409149	HS_5066_A
73	246	64.4	567	AO545189	CITBI-EI-
74	245.2	64.2	467	AO428869	CITBI-EI-
75	245.2	64.2	507	AO596757	HS_5206_A
76	245.2	64.2	654	AO423408	CITBI-EI-
77	244.6	64.0	428	W74578	z476f10.r1
78	244.4	64.0	428	AO206677	HS_3240_A
79	244.4	64.0	706	AO782398	HS_3106_A
80	244	63.9	393	AO181082	HS_3218_A
81	243.8	63.8	467	AA7442978	ny15e12.s
82	243.8	63.8	435	AI673314	ts81b01.x
83	243.8	63.8	519	AI635524	ts91d02.x
84	243.8	63.8	664	AG156971	Pan t1091
85	243.8	63.8	844	AO781691	HS_3106_A
86	243.6	63.8	426	AO685236	HS_5515_A
87	243	63.6	521	AO536324	RPCI-11-3
88	242.6	63.5	477	AO335001	HS_5012_B
89	242.4	63.5	565	AO630428	RPCI-11-4
90	242	63.4	582	AO428865	CITBI-EI-
91	242	63.4	603	AO590605	HS_5398_A
92	241.8	63.3	521	AO753922	HS_5398_A
93	241.8	63.3	560	AO508987	RPCI-11-2
94	241.6	63.2	441	AO377070	RPCI11-15
95	241.2	63.1	557	AO734463	HS_3012_A
96	241.2	63.1	852	AO751669	HS_3568_B
97	240.4	62.9	396	AO534062	RPCI-11-3

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 248.866 Seconds  
(without alignments)  
9130.760 Million cell updates/sec

Title: US-09-854-867-4

Perfect score: 382  
Sequence: 1 ctgcagacactactccag.....ctgtccctccatcagatc 382

Scoring table:

IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database:

Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCNT\_NEW\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
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18: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	382	10	US-09-854-867-4
2	364.4	95.4	1959	9	US-09-864-761-3814
3	306.6	80.3	538	13	US-10-027-632-235922
4	306.6	80.3	538	13	US-10-027-632-235923
5	306.6	80.3	538	13	US-10-027-632-235924
6	306.6	80.3	538	17	US-10-027-632-235923
7	306.6	80.3	538	17	US-10-027-632-235923
8	306.6	80.3	538	17	US-10-027-632-235924
9	278.6	72.9	1002	16	US-10-029-386-25469
10	274.8	71.9	2771	17	US-10-104-047-1081
11	267.4	70.0	672	9	US-09-864-761-20580

Sequence 3814, App1  
Sequence 235922,  
Sequence 235923,  
Sequence 235924,  
Sequence 235923,  
Sequence 235923,  
Sequence 235923,  
Sequence 235924,  
Sequence 25469, A  
Sequence 1081, Ap  
Sequence 20580, A

C 12	260.4	68.2	509	9	US-09-864-761-18463	Sequence 18463, A
C 13	260.4	68.2	575	16	US-10-029-386-1189	Sequence 1189, Ap
C 14	255.6	66.9	525	16	US-10-029-386-3654	Sequence 3654, Ap
C 15	255.6	66.9	591	16	US-10-029-386-3599	Sequence 3599, Ap
C 16	255	66.8	505	16	US-10-029-386-3729	Sequence 3729, Ap
C 17	254	66.5	624	13	US-10-027-632-193860	Sequence 193860,
C 18	254	66.5	624	17	US-10-027-632-193860	Sequence 193860,
C 19	250.8	65.7	527	9	US-09-864-761-8023	Sequence 8023, Ap
C 20	248.8	65.1	524	16	US-10-029-386-11769	Sequence 11769, A
C 21	248.2	65.0	572	16	US-10-029-386-22602	Sequence 22602, A
C 22	246.6	64.6	542	16	US-10-029-386-6571	Sequence 6571, Ap
C 23	246.2	64.5	560	13	US-10-027-632-238047	Sequence 238047,
C 24	246.2	64.5	560	13	US-10-027-632-238048	Sequence 238048,
C 25	246.2	64.5	560	13	US-10-027-632-238049	Sequence 238049,
C 26	246.2	64.5	560	13	US-10-027-632-238050	Sequence 238050,
C 27	246.2	64.5	560	17	US-10-027-632-238047	Sequence 238047,
C 28	246.2	64.5	560	17	US-10-027-632-238048	Sequence 238048,
C 29	246.2	64.5	560	17	US-10-027-632-238049	Sequence 238049,
C 30	246.2	64.5	560	17	US-10-027-632-238050	Sequence 238050,
C 31	245.6	64.3	492	9	US-09-864-761-1708	Sequence 1708, Ap
C 32	242.8	63.6	454	16	US-10-029-386-20535	Sequence 20535, A
C 33	242.8	63.6	1055	16	US-10-029-386-22726	Sequence 22726, A
C 34	242.4	63.5	438	13	US-10-027-632-183614	Sequence 183614,
C 35	242.4	63.5	438	13	US-10-027-632-183615	Sequence 183615,
C 36	242.4	63.5	438	13	US-10-027-632-183616	Sequence 183616,
C 37	242.4	63.5	438	17	US-10-027-632-183614	Sequence 183614,
C 38	242.4	63.5	438	17	US-10-027-632-183615	Sequence 183615,
C 39	242.4	63.5	438	17	US-10-027-632-183616	Sequence 183616,
C 40	241.2	63.1	496	16	US-10-029-386-20298	Sequence 20298, A
C 41	241.2	63.1	521	16	US-10-029-386-11765	Sequence 11765, A
C 42	241.2	63.1	530	13	US-10-027-632-60201	Sequence 60201, A
C 43	241.2	63.1	530	13	US-10-027-632-60201	Sequence 60201, A
C 44	241.2	63.1	832	16	US-10-029-386-25323	Sequence 25323, A
C 45	241.2	63.1	853	16	US-10-029-386-22940	Sequence 22940, A
C 46	241	63.1	504	13	US-10-027-632-214204	Sequence 214204,
C 47	241	63.1	504	13	US-10-027-632-214205	Sequence 214205,
C 48	241	63.1	504	17	US-10-027-632-214204	Sequence 214204,
C 49	241	63.1	504	17	US-10-027-632-214205	Sequence 214205,
C 50	238.8	62.5	637	13	US-10-027-632-245373	Sequence 245373,
C 51	238.8	62.5	637	13	US-10-027-632-245374	Sequence 245374,
C 52	238.8	62.5	637	17	US-10-027-632-245373	Sequence 245373,
C 53	238.8	62.5	637	17	US-10-027-632-245374	Sequence 245374,
C 54	238.4	62.4	546	13	US-10-027-632-194756	Sequence 194756,
C 55	238.4	62.4	546	13	US-10-027-632-194757	Sequence 194757,
C 56	238.4	62.4	546	13	US-10-027-632-194758	Sequence 194758,
C 57	238.4	62.4	546	17	US-10-027-632-194757	Sequence 194757,
C 58	238.4	62.4	546	17	US-10-027-632-194758	Sequence 194758,
C 59	238.4	62.4	546	17	US-10-027-632-194757	Sequence 194757,
C 60	237.2	62.1	581	13	US-10-027-632-95663	Sequence 95663, A
C 61	237.2	62.1	581	13	US-10-027-632-95663	Sequence 95663, A
C 62	237.2	62.1	581	13	US-10-027-632-95664	Sequence 95664, A
C 63	237.2	62.1	581	13	US-10-027-632-95663	Sequence 95663, A
C 64	237.2	62.1	581	13	US-10-027-632-95664	Sequence 95664, A
C 65	237.2	62.1	581	17	US-10-027-632-318763	Sequence 318763,
C 66	237.2	62.1	581	17	US-10-027-632-318764	Sequence 318764,
C 67	237.2	62.1	581	17	US-10-027-632-318765	Sequence 318765,
C 68	237.2	62.1	581	17	US-10-027-632-318766	Sequence 318766,
C 69	237.2	62.1	581	17	US-10-027-632-318767	Sequence 318767,
C 70	237.2	62.1	581	17	US-10-027-632-318768	Sequence 318768,
C 71	237.2	62.1	581	17	US-10-027-632-318769	Sequence 318769,
C 72	236.8	62.0	595	13	US-10-027-632-221958	Sequence 221958,
C 73	236.8	62.0	595	13	US-10-027-632-221959	Sequence 221959,
C 74	236.8	62.0	595	17	US-10-027-632-221958	Sequence 221958,
C 75	236.8	62.0	595	17	US-10-027-632-221959	Sequence 221959,
C 76	236.4	61.9	2896	17	US-10-108-2604-987	Sequence 987, App
C 77	236	61.8	533	13	US-10-027-632-80624	Sequence 80624, A
C 78	236	61.8	533	13	US-10-027-632-80624	Sequence 80624, A
C 79	234.8	61.5	532	16	US-10-029-386-9239	Sequence 9239, Ap
C 80	233.6	61.2	520	13	US-10-027-632-248095	Sequence 248095,
C 81	233.6	61.2	520	13	US-10-027-632-248097	Sequence 248097,
C 82	233.6	61.2	520	13	US-10-027-632-248095	Sequence 248095,
C 83	233.6	61.2	520	17	US-10-027-632-248095	Sequence 248095,
C 84	233.6	61.2	520	17	US-10-027-632-248096	Sequence 248096,

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 69.6062 Seconds

(without alignments)  
8979.909 Million cell updates/sec

Title: US-09-854-867-4

Perfect score: 382  
Sequence: 1 ctgcagacactactccag.....ctgtccctcacatagaattc 382

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: Issued Patents NA.\*  
2: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	382	4	US-09-573-080A-4
2	38.4	10.1	83617	4	US-09-949-016-12254
3	38	9.9	36223	4	US-09-949-016-14417
4	35.2	9.2	2407	4	US-09-023-655-812
5	33.2	8.7	221958	4	US-09-949-016-12173
6	33.2	8.7	221966	4	US-09-949-016-15498
7	32.6	8.5	43018	4	US-09-949-016-12265
8	32.6	8.5	43095	4	US-09-949-016-17530
9	32.4	8.5	957	3	US-09-123-912-113
10	32.4	8.5	957	3	US-09-643-597-113
11	32.4	8.5	957	4	US-09-480-884A-113
12	32.4	8.5	957	4	US-09-542-615A-113
13	32.4	8.5	957	4	US-09-606-421B-113
14	32.4	8.5	957	4	US-09-221-107-113
15	32.4	8.5	957	4	US-09-466-396A-113
16	32.4	8.5	957	4	US-09-476-496A-113
17	32.4	8.5	957	4	US-09-630-940B-113
18	32.4	8.5	957	4	US-09-285-479-113
19	32.4	8.5	1497	4	US-09-230-132-94
20	32.4	8.5	58356	4	US-09-949-016-15553
21	32.2	8.4	601	4	US-09-949-016-12691
22	32.2	8.4	601	4	US-09-949-016-12691
23	32.2	8.4	137394	4	US-09-949-016-13872
24	32.2	8.4	137743	4	US-09-949-016-12178
25	31.8	8.3	601	4	US-09-949-016-12692
26	31.8	8.3	118141	4	US-09-949-016-17196
27	31.6	8.3	601	4	US-09-949-016-15068

28	31.6	8.3	28358	4	US-09-949-016-13506	Sequence 13506, A
29	31.4	8.2	60110	4	US-09-949-016-17338	Sequence 17338, A
30	31.4	8.2	60110	4	US-09-949-016-17338	Sequence 17339, A
31	31.4	8.2	61083	4	US-09-949-016-14144	Sequence 14144, A
32	31.4	8.2	61083	4	US-09-949-016-14145	Sequence 14145, A
33	31.2	8.2	601	4	US-09-949-016-179097	Sequence 179097, A
34	31.2	8.2	13595	4	US-09-949-016-12529	Sequence 12529, A
35	31.2	8.2	13970	4	US-09-949-016-16910	Sequence 16910, A
36	31.2	8.2	59479	4	US-09-949-016-16910	Sequence 16910, A
37	31	8.1	382	4	US-09-573-080A-4	Sequence 4, Appl
38	31	8.1	601	4	US-09-949-016-68262	Sequence 68262, A
39	31	8.1	601	4	US-09-949-016-68263	Sequence 68263, A
40	31	8.1	132456	4	US-09-949-016-13750	Sequence 13750, A
41	31	8.1	247299	4	US-09-949-016-17590	Sequence 17590, A
42	30.6	8.0	19826	4	US-09-949-016-16973	Sequence 16973, A
43	30.6	8.0	28198	4	US-09-949-016-12349	Sequence 12349, A
44	30.6	8.0	14635	4	US-09-949-016-13927	Sequence 13927, A
45	30.2	7.9	15478	4	US-09-949-016-12529	Sequence 12529, A
46	30.2	7.9	15478	4	US-09-949-016-15288	Sequence 15288, A
47	30	7.9	601	4	US-09-949-016-198083	Sequence 198083, A
48	30	7.9	2376	1	US-07-912-952-3	Sequence 3, Appl
49	30	7.9	24020	4	US-09-949-016-17353	Sequence 17353, A
50	29.8	7.8	31623	4	US-09-949-016-15945	Sequence 15945, A
51	29.8	7.8	56678	4	US-09-949-016-17453	Sequence 17453, A
52	29.8	7.8	149543	4	US-09-949-016-17573	Sequence 17573, A
53	29.6	7.7	322	4	US-09-513-999C-17698	Sequence 17698, A
54	29.6	7.7	601	4	US-09-949-016-120621	Sequence 120621, A
55	29.6	7.7	18349	4	US-09-949-016-14463	Sequence 14463, A
56	29.6	7.7	145812	4	US-09-949-016-15698	Sequence 15698, A
57	29.6	7.7	209210	4	US-09-949-016-15094	Sequence 15094, A
58	29.4	7.7	601	4	US-09-949-016-37902	Sequence 37902, A
59	29.4	7.7	601	4	US-09-949-016-142690	Sequence 142690, A
60	29.4	7.7	1844	3	US-09-643-597-88	Sequence 88, Appl
61	29.4	7.7	1844	3	US-09-643-597-88	Sequence 88, Appl
62	29.4	7.7	1844	4	US-09-480-884A-88	Sequence 88, Appl
63	29.4	7.7	1844	4	US-09-542-615A-88	Sequence 88, Appl
64	29.4	7.7	1844	4	US-09-606-421B-88	Sequence 88, Appl
65	29.4	7.7	1844	4	US-09-476-496A-88	Sequence 88, Appl
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67	29.4	7.7	1844	4	US-09-466-396A-88	Sequence 88, Appl
68	29.4	7.7	1844	4	US-09-476-496A-88	Sequence 88, Appl
69	29.4	7.7	1844	4	US-09-630-940B-88	Sequence 88, Appl
70	29.4	7.7	1844	4	US-09-285-479-88	Sequence 88, Appl
71	29.4	7.7	3134	1	US-07-865-662F-7	Sequence 7, Appl
72	29.4	7.7	32721	4	US-08-374-219B-7	Sequence 7, Appl
73	29.4	7.7	90618	4	US-09-949-016-14100	Sequence 14100, A
74	29.4	7.7	112705	4	US-09-949-016-15630	Sequence 15630, A
75	29.4	7.7	112705	4	US-09-949-016-15630	Sequence 15630, A
76	29.4	7.7	112705	4	US-09-949-016-15630	Sequence 15630, A
77	29.2	7.6	601	4	US-09-949-016-15775	Sequence 15775, A
78	29.2	7.6	601	4	US-09-949-016-73529	Sequence 73529, A
79	29.2	7.6	601	4	US-09-949-016-143710	Sequence 143710, A
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81	29.2	7.6	55135	4	US-09-949-016-15766	Sequence 15766, A
82	29.2	7.6	69199	4	US-09-949-016-16887	Sequence 16887, A
83	29.2	7.6	421491	4	US-09-949-016-13881	Sequence 13881, A
84	29.2	7.6	421494	4	US-09-949-016-12805	Sequence 12805, A
85	29.2	7.6	601	4	US-09-949-016-14402	Sequence 14402, A
86	29	7.6	45229	4	US-09-949-016-14402	Sequence 14402, A
87	29	7.6	45229	4	US-09-949-016-13228	Sequence 13228, A
88	29	7.6	105050	4	US-09-949-016-15353	Sequence 15353, A
89	29	7.6	133613	4	US-09-949-016-15824	Sequence 15824, A
90	29	7.6	174170	4	US-09-949-016-14810	Sequence 14810, A
91	29	7.6	174170	4	US-09-949-016-14811	Sequence 14811, A
92	29	7.6	174170	4	US-09-949-016-14811	Sequence 14811, A
93	29	7.6	174170	4	US-09-949-016-14812	Sequence 14812, A
94	29	7.6	174170	4	US-09-949-016-14812	Sequence 14812, A
95	29	7.6	174170	4	US-09-949-016-12417	Sequence 12417, A
96	29	7.6	174170	4	US-09-949-016-12417	Sequence 12417, A
97	28.8	7.5	453	4	US-09-543-681A-4017	Sequence 4017, Ap
98	28.8	7.5	601	4	US-09-949-016-32510	Sequence 32510, A
99	28.8	7.5	601	4	US-09-949-016-32510	Sequence 32510, A
100	28.8	7.5	601	4	US-09-949-016-32511	Sequence 32511, A

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:44:41 ; Search time 229.319 Seconds  
(without alignments)  
9861.108 Million cell updates/sec

Title: US-09-854-867-4  
Perfect score: 382  
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Scoring table:  
IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
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12: geneeqn2000s:\*  
13: geneeqn2000s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	382	7	AD530971 Human gen
2	364.4	95.4	1959	4	AA135309 Probe #39
3	364.4	95.4	1959	4	ABA45170 Human bre
4	364.4	95.4	1959	4	ABA25348 Probe #38
5	364.4	95.4	1959	4	AAK03877 Human bra
6	364.4	95.4	1959	6	ABS28968 Human liv
7	364.4	95.4	1959	6	ABS03907 Human gen
8	278.6	72.9	1002	12	ACH92274 Human gen
9	278.6	72.9	6477	5	AA568898 DNA encod
10	274.8	71.9	2771	10	AD562927 Human gen
11	267.4	70.0	672	4	AA148466 Probe #17
12	267.4	70.0	672	4	ABA50306 Human bre
13	267.4	70.0	672	4	ABA53260 Probe #13
14	267.4	70.0	672	4	AAK16627 Human liv
15	267.4	70.0	672	4	ABA41996 Human bra
16	267.4	70.0	672	6	ABS16442 Human gen
17	260.4	68.2	509	4	AA120995 Probe #10
18	260.4	68.2	509	4	ABA66063 Human foe
19	260.4	68.2	509	4	AA146244 Probe #14
20	260.4	68.2	509	4	ABA48185 Human bre

C	21	260.4	68.2	509	4	ABA33143	ABA33143 Probe #11
C	22	260.4	68.2	509	4	AAK40229	AAK40229 Human bon
C	23	260.4	68.2	509	4	AAK14487	AAK14487 Human bra
C	24	260.4	68.2	509	4	ABS39806	ABS39806 Human liv
C	25	260.4	68.2	509	5	AA106707	AA106707 Probe #66
C	26	260.4	68.2	509	6	ABS14270	ABS14270 Human gen
C	27	260.4	68.2	575	12	ACH67994	ACH67994 Human gen
C	28	260.4	68.2	2436	5	AA570526	AA570526 DNA encod
C	29	256.2	67.1	2448	5	AA567750	AA567750 DNA encod
C	30	255.8	67.0	756	12	ADN99992	ADN99992 Novel hum
C	31	255.8	67.0	756	12	ADN98424	ADN98424 Novel hum
C	32	255.6	66.9	525	12	ACH70459	ACH70459 Human gen
C	33	255.6	66.9	525	12	ACH70404	ACH70404 Human gen
C	34	255	66.8	505	12	ACH70534	ACH70534 Human gen
C	35	254	66.5	1055	5	AA569705	AA569705 DNA encod
C	36	250.8	65.7	527	4	ABA52174	ABA52174 Human foe
C	37	250.8	65.7	527	4	AA142128	AA142128 Probe #80
C	38	250.8	65.7	527	4	ABA29557	ABA29557 Probe #10
C	39	250.8	65.7	527	4	AAK36394	AAK36394 Human bon
C	40	250.8	65.7	527	4	AAK10495	AAK10495 Human bra
C	41	250.8	65.7	527	4	ABS36069	ABS36069 Human liv
C	42	248.8	65.1	524	12	ACH78574	ACH78574 Human gen
C	43	248.2	65.0	572	12	ACH89407	ACH89407 Human gen
C	44	246.6	64.6	542	12	ACH73376	ACH73376 Human gen
C	45	245.6	64.3	492	4	AA111783	AA111783 Probe #17
C	46	245.6	64.3	492	4	ABA53473	ABA53473 Human foe
C	47	245.6	64.3	492	4	AA133095	AA133095 Probe #17
C	48	245.6	64.3	492	4	ABA43059	ABA43059 Human bre
C	49	245.6	64.3	492	4	ABA23242	ABA23242 Probe #17
C	50	245.6	64.3	492	4	AAK27200	AAK27200 Human bon
C	51	245.6	64.3	492	4	AAK01745	AAK01745 Human bra
C	52	245.6	64.3	492	4	ABS26780	ABS26780 Human liv
C	53	245.6	64.3	492	5	AA101712	AA101712 Probe #17
C	54	245.6	64.3	492	5	ABS01743	ABS01743 Human gen
C	55	244.4	64.0	1342	5	AA570666	AA570666 DNA encod
C	56	242.8	63.6	454	12	ACH87340	ACH87340 Human gen
C	57	242.8	63.6	1055	12	ACH89531	ACH89531 Human gen
C	58	241.2	63.1	496	12	ACH87103	ACH87103 Human gen
C	59	241.2	63.1	521	12	ACH78570	ACH78570 Human gen
C	60	241.2	63.1	832	12	ACH92128	ACH92128 Human gen
C	61	241.2	63.1	833	12	ACH89745	ACH89745 Human gen
C	62	238.8	62.5	965	5	AA580774	AA580774 DNA encod
C	63	236.4	61.9	2896	11	ADM02302	ADM02302 Human gen
C	64	234.8	61.5	532	12	ACH76044	ACH76044 Human gen
C	65	233.2	61.0	615	12	ACH92054	ACH92054 Human gen
C	66	232.8	60.9	882	12	ACH89517	ACH89517 Human gen
C	67	231.2	60.5	1002	12	ADN99993	ADN99993 Novel hum
C	68	231.2	60.5	1002	12	ADN98425	ADN98425 Novel hum
C	69	231.2	60.5	386	4	ABA74668	ABA74668 Human foe
C	70	231	60.5	386	4	AA155161	AA155161 Probe #23
C	71	231	60.5	386	4	ABA39407	ABA39407 Probe #17
C	72	231	60.5	386	4	AAK49314	AAK49314 Human bon
C	73	231	60.5	386	4	AAK23141	AAK23141 Human bra
C	74	231	60.5	386	4	ABS48953	ABS48953 Human liv
C	75	228.6	59.8	519	12	ACH90996	ACH90996 Human gen
C	76	228.6	59.8	518	12	ACH75824	ACH75824 Human gen
C	77	228.4	59.8	524	12	ACH78347	ACH78347 Human gen
C	78	225.2	59.0	572	12	ACH92271	ACH92271 Human gen
C	79	225.2	59.0	885	12	ACH89540	ACH89540 Human gen
C	80	221.2	57.9	533	12	ACH75799	ACH75799 Human gen
C	81	220	57.6	1098	5	AA570933	AA570933 DNA encod
C	82	218.4	57.2	600	12	ADN99996	ADN99996 Novel hum
C	83	218.4	57.2	600	12	ADN98428	ADN98428 Novel hum
C	84	217.4	56.9	566	12	ACH78423	ACH78423 Human gen
C	85	217.2	56.9	327	12	ACH81696	ACH81696 Human gen
C	86	213.6	55.9	580	12	ACH75683	ACH75683 Human gen
C	87	213.4	55.9	566	12	ACH77296	ACH77296 Human gen
C	88	211.4	55.3	532	12	ACH73626	ACH73626 Human gen
C	89	202.6	53.0	308	12	ACH84234	ACH84234 Human gen
C	90	200.8	52.6	343	3	AA26463	AA26463 Human ORF
C	91	195.6	51.2	549	12	ACH75813	ACH75813 Human gen
C	92	195.2	51.1	559	6	AB058182	AB058182 Human COI
C	93	183.4	48.0	261	12	ACH84104	ACH84104 Human gen

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 1752.31 Seconds

(without alignments) 10563.118 Million cell updates/sec

Title: US-09-854-867-4

Perfect score: 382

Sequence: 1 ctgcagacactactctcag.....ctgcctccatagatc 382

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database:

GenBankl: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_bcs: \*  
12: gb\_by: \*  
13: gb\_un: \*  
14: gb\_vl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	382	9 HUMREP	M27785 Human D2223
2	377.2	98.7	213227	9 AC138772	AC138772 Homo sapi
3	375.6	98.3	157733	9 AC138771	AC138771 Homo sapi
4	375.6	98.3	165081	2 CR382332	CR382332 Homo sapi
5	375.6	98.3	216075	2 AC138777	AC138777 Homo sapi
6	374	97.9	110000	2 BX511044_0	BX511044 Homo sapi
7	374	97.9	191109	2 AC027456	AC027456 Homo sapi
8	374	97.9	201709	9 BX004987	BX004987 Human DNA
9	370.8	97.1	484	9 HUMSNOWA	M76594 Homo sapien
10	367.6	96.2	151418	2 AC025100	AC025100 Homo sapi
11	366	95.8	183261	2 AC148028	AC148028 Homo sapi
12	366	95.8	191469	9 AC145212	AC145212 Homo sapi
13	364.4	95.4	1959	6 CO095136	CO095136 Sequence
14	364.4	95.4	1959	6 CO172418	CO172418 Sequence
15	364.4	95.4	1959	6 CO201588	CO201588 Sequence
16	364.4	95.4	1959	6 CO217119	CO217119 Sequence
17	364.4	95.4	1959	6 CO292793	CO292793 Sequence
18	364.4	95.4	1959	6 CO329774	CO329774 Sequence
19	364.4	95.4	114546	2 HSNAC00382	AC000382 Homo sapi

20	332.4	87.0	110000	2 BX511044_2	BX511044_2
21	332.4	87.0	110898	9 AL355973	AL355973 Human DNA
22	330.8	86.6	152296	9 CR381535	CR381535 Human DNA
23	330.8	86.6	158069	9 CR392039	CR392039 Human DNA
24	330.8	86.6	208765	9 AC118282	AC118282 Homo sapi
25	329.2	86.2	102530	2 AC147060	AC147060 Homo sapi
26	329.2	86.2	136511	2 AC145621	AC145621 Homo sapi
27	329.2	86.2	145618	2 AC026079	AC026079 Homo sapi
28	329.2	86.2	145618	2 AC024235	AC024235 Homo sapi
29	329.2	86.2	152777	2 AC027762	AC027762 Homo sapi
30	329.2	86.2	155655	2 AC140113	AC140113 Homo sapi
31	329.2	86.2	155813	9 AC134878	AC134878 Homo sapi
32	329.2	86.2	167426	2 AC091085	AC091085 Homo sapi
33	329.2	86.2	171176	2 AC119751	AC119751 Homo sapi
34	309.4	81.0	165731	9 BX640538	BX640538 Human DNA
35	309.4	81.0	167647	2 AC148024	AC148024 Homo sapi
36	309.4	81.0	302859	2 AC044785	AC044785 Homo sapi
37	305.8	80.1	66797	2 AC084718	AC084718 Homo sapi
38	305.8	80.1	190724	2 AC078877	AC078877 Homo sapi
39	304.2	79.6	160460	2 AC024374	AC024374 Homo sapi
40	304.2	79.6	161536	2 AC024318	AC024318 Homo sapi
41	304.2	79.6	179693	9 AL591856	AL591856 Human DNA
42	304.2	79.6	192016	2 AC026540	AC026540 Homo sapi
43	288.2	75.4	110000	2 BX511044_3	BX511044_3
44	288.2	75.4	127682	9 AL137861	AL137861 Human DNA
45	288.2	75.4	133948	2 BX322233	BX322233 Homo sapi
46	286.6	75.0	194050	9 AC138774	AC138774 Homo sapi
47	286.6	74.9	86723	9 AF401203	AF401203 Homo sapi
48	286.6	74.9	161147	9 AL354832	AL354832 Human DNA
49	282.8	74.0	195588	9 AL583842	AL583842 Homo sapi
50	280.6	73.5	129414	2 AC068398	AC068398 Homo sapi
51	279.6	73.2	127105	2 AC011881	AC011881 Homo sapi
52	279.6	73.2	210656	9 AC138775	AC138775 Homo sapi
53	276.4	72.4	160460	2 AC024374	AC024374 Homo sapi
54	276.4	72.4	161536	2 AC024318	AC024318 Homo sapi
55	274.8	71.9	2271	6 AX747556	AX747556 Sequence
56	274.8	71.9	2771	9 AK092459	AK092459 Homo sapi
57	274.8	71.9	155662	2 AC024454	AC024454 Homo sapi
58	274.8	71.9	164562	2 AC027471	AC027471 Homo sapi
59	274.8	71.9	202926	9 AC138776	AC138776 Homo sapi
60	273.2	71.5	3189	9 AF402806	AF402806 Homo sapi
61	273.2	71.5	114080	9 AC133123	AC133123 Homo sapi
62	273.2	71.5	155397	9 AL590523	AL590523 Human DNA
63	273.2	71.5	165333	9 BX546492	BX546492 Human DNA
64	273.2	71.5	186739	9 BX572084	BX572084 Human DNA
65	273.2	71.5	191144	9 AC138773	AC138773 Homo sapi
66	271.6	71.1	40247	2 AC145662	AC145662 Homo sapi
67	271.6	71.1	41343	9 AC145652	AC145652 Homo sapi
68	271.6	71.1	128909	2 CR381653	CR381653 Homo sapi
69	271.6	71.1	175055	9 BX571672	BX571672 Human DNA
70	271.6	71.1	183417	2 AC068832	AC068832 Homo sapi
71	271.6	71.1	192016	2 AC026540	AC026540 Homo sapi
72	270	70.7	57789	2 AC091570	AC091570 Homo sapi
73	270	70.7	129889	9 CR381670	CR381670 Human DNA
74	270	70.7	185235	2 AC012661	AC012661 Homo sapi
75	269	70.7	186661	9 AL592170	AL592170 Human DNA
76	269	70.4	186773	9 AC108724	AC108724 Homo sapi
77	268.6	70.3	155958	2 AC024975	AC024975 Homo sapi
78	268.6	70.3	110000	2 BX511044_4	BX511044_4
79	268.6	70.3	160669	2 AC023586	AC023586 Homo sapi
80	268.4	70.3	190724	2 AC078877	AC078877 Homo sapi
81	267.4	70.0	672	6 AC0108293	AC0108293 Sequence
82	267.4	70.0	672	6 CO182330	CO182330 Sequence
83	267.4	70.0	672	6 CO206724	CO206724 Sequence
84	267.4	70.0	672	6 CO230147	CO230147 Sequence
85	267.4	70.0	672	6 CO305328	CO305328 Sequence
86	267.4	70.0	672	6 CO342524	CO342524 Sequence
87	267	69.9	176111	2 AC067789	AC067789 Homo sapi
88	266.8	69.8	142616	2 AC067789	AC067789 Homo sapi
89	266.8	69.8	142616	2 AC067789	AC067789 Homo sapi
90	266.8	69.8	183417	2 AC068832	AC068832 Homo sapi
91	266.4	69.7	177110	2 AC133042	AC133042 Homo sapi
92	266.2	69.7	174588	9 AC011841	AC011841 Homo sapi

Continuation (3 of 3)  
AL355973 Human DNA  
CR381535 Human DNA  
CR392039 Human DNA  
AC118282 Homo sapi  
AC147060 Homo sapi  
AC145621 Homo sapi  
AC026079 Homo sapi  
AC024235 Homo sapi  
AC027762 Homo sapi  
AC140113 Homo sapi  
AC134878 Homo sapi  
AC091085 Homo sapi  
AC119751 Homo sapi  
BX640538 Human DNA  
AC148024 Homo sapi  
AC044785 Homo sapi  
AC084718 Homo sapi  
AC078877 Homo sapi  
AC024374 Homo sapi  
AC024318 Homo sapi  
AL591856 Human DNA  
AC026540 Homo sapi  
Continuation (4 of 4)  
AL137861 Human DNA  
BX322233 Homo sapi  
AC138774 Homo sapi  
AF401203 Homo sapi  
AL354832 Human DNA  
AL583842 Homo sapi  
AC068398 Homo sapi  
AC011881 Homo sapi  
AC138775 Homo sapi  
AC024374 Homo sapi  
AC024318 Homo sapi  
AX747556 Sequence  
AK092459 Homo sapi  
AC024454 Homo sapi  
AC027471 Homo sapi  
AC138776 Homo sapi  
AF402806 Homo sapi  
AC133123 Homo sapi  
AL590523 Human DNA  
BX546492 Human DNA  
BX572084 Human DNA  
AC138773 Homo sapi  
AC145662 Homo sapi  
AC145652 Homo sapi  
CR381653 Homo sapi  
BX571672 Human DNA  
AC068832 Homo sapi  
AC026540 Homo sapi  
AC091570 Homo sapi  
CR381670 Human DNA  
AC012661 Homo sapi  
AL592170 Human DNA  
AC108724 Homo sapi  
AC024975 Homo sapi  
Continuation (5 of 5)  
AC023586 Homo sapi  
AC078877 Homo sapi  
AC0108293 Sequence  
CO182330 Sequence  
CO206724 Sequence  
CO230147 Sequence  
CO305328 Sequence  
CO342524 Sequence  
AC067789 Homo sapi  
AC067789 Homo sapi  
AC067789 Homo sapi  
AC068832 Homo sapi  
AC133042 Homo sapi  
AC011841 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:09:22 ; Search time 258.177 Seconds

(without alignments)  
10025.556 Million cell updates/sec

Title: US-09-854-867-3

Perfect score: 68  
Sequence: 1 gctcagtgagagagatcgtc.....aagagttacatcacctgggt 68

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.6	90.6	173	6	CD164663 M1-0090T
2	61.6	90.6	335	6	AG266749 Homo sapi
3	60.6	89.1	616	8	AG555124 RPT1-11-3
4	60.6	88.2	943	8	AG743035 HS_5387_B
5	60.6	88.2	400	8	AG621521 HS_3030_B
6	60.6	88.2	411	8	AG016754 CTF-HSP-2
7	60.6	88.2	470	8	AG0789316 HS_3250_A
8	60.6	88.2	532	8	AG508622 RPT1-11-3
9	60.6	88.2	536	8	AG466364 HS_5153_B
10	60.6	88.2	617	1	AA174078 AA174078
11	60.6	88.2	718	8	AG897999 HS_3122_B
12	60.6	88.2	777	8	AG749728 HS_5573_A
13	60.6	88.2	844	8	AG746068 HS_2277_A
14	60.6	88.2	959	8	AG747420 HS_5537_A
15	58.4	85.9	116	6	CD086997 MCI-0034T
16	58.4	85.9	248	2	BE045056 hm26e10.x
17	58.4	85.9	319	9	AG265802 Homo sapi
18	58.4	85.9	338	8	AG279828 CITR1-E1-
19	58.4	85.9	446	8	AG357456 CITR1-E1-
20	58.4	85.9	476	8	AG165121 HS_3032_B
21	58.4	85.9	491	8	AG880166 HS_5037_B
22	58.4	85.9	506	8	AG149095 HS_3165_A
23	58.4	85.9	518	8	AG165428 HS_3031_A
24	58.4	85.9	529	8	AG784754 HS_3249_A

25	58.4	85.9	538	8	AG333667 HS_5013_A
26	58.4	85.9	547	8	AG279387 CITR1-E1-
27	58.4	85.9	566	8	AG260254 CITR1-E1-
28	58.4	85.9	567	8	AG355370 CITR1-E1-
29	58.4	85.9	575	8	AG251854 RPT1-11-1
30	58.4	85.9	600	8	AG263555 CITR1-E1-
31	58.4	85.9	840	8	AG897026 HS_3153_A
32	58.4	85.9	853	8	AG787779 HS_3072_A
33	58.4	85.9	1093	8	AF139717 AF139717
34	57.4	84.4	343	8	AG083344
35	57.4	84.4	541	8	AG144422 HS_3084_A
36	57.4	84.4	555	2	AG063430
37	57.4	84.4	511	8	AG482389 RPT1-11-2
38	57.4	84.4	556	8	AG784087 HS_3250_A
39	56.8	83.5	339	9	AG266279 Homo sapi
40	56.8	83.5	341	8	AG028509 CIT-HSP-2
41	56.8	83.5	415	8	AG173952 HS_3204_A
42	56.8	83.5	451	1	AG289438
43	56.8	83.5	465	8	AG080519 HS_3141_A
44	56.8	83.5	509	8	AG498992 HS_5154_B
45	56.8	83.5	522	8	AG090999 HS_3251_A
46	56.8	83.5	542	8	AG545641 CITR1-E1-
47	56.8	83.5	549	8	AG547110 RPT1-11-4
48	56.8	83.5	557	8	AG428667 CITR1-E1-
49	56.8	83.5	558	8	AG488499 RPT1-11-2
50	56.8	83.5	564	8	AG769339 HS_3156_A
51	56.8	83.5	589	8	AG387826 RPT1-11-15
52	56.8	83.5	599	8	AG312295 RPT1-11-10
53	56.8	83.5	609	8	AG897013 HS_3153_A
54	56.8	83.5	617	8	AG380528 RPT1-11-16
55	56.8	83.5	840	8	AG098658 HS_3129_B
56	56.8	83.5	894	8	AG098657 HS_3129_B
57	56.4	82.9	201	8	AG583739 RPT1-11-4
58	56.4	82.9	344	8	AG066172 CITR1-E1-
59	56.4	82.9	660	8	AG28361 CITR1-E1-
60	55.8	82.1	669	8	AG112283 RPT1-11-10
61	55.4	81.5	283	2	BE009212 CM3-BN016
62	55.2	81.5	415	8	AG453368 HS_5192_A
63	55.2	81.2	138	2	AG63292 MR3-SN000
64	55.2	81.2	308	2	AG51265 IL3-CT022
65	55.2	81.2	308	2	AG51265 IL3-CT022
66	55.2	81.2	339	9	AG65952 Homo sapi
67	55.2	81.2	345	9	AG265844 Homo sapi
68	55.2	81.2	380	8	AG277886 CITR1-E1-
69	55.2	81.2	381	8	AG0203294 HS_3239_A
70	55.2	81.2	391	8	AG095474 HS_3034_A
71	55.2	81.2	410	8	AG471830 CITR1-E1-
72	55.2	81.2	413	8	AG278058 CITR1-E1-
73	55.2	81.2	430	8	AG211059 HS_3234_B
74	55.2	81.2	434	8	AG260253 CITR1-E1-
75	55.2	81.2	469	8	AG42961 HS-1056-B2-
76	55.2	81.2	517	8	AG477082 CITR1-E1-
77	55.2	81.2	542	8	AG085373 HS_5531_B
78	55.2	81.2	550	8	AG265844 Homo sapi
79	55.2	81.2	647	8	AG392523 CITR1-E1-
80	55.2	81.2	658	8	AG418369 RPT1-11-1
81	55.2	81.2	685	8	AG424085 CITR1-E1-
82	55.2	81.2	780	8	AG098000 HS_3122_B
83	55.2	81.2	844	8	AG746350 HS_2277_A
84	55.2	81.2	860	8	AG781811 HS_3148_A
85	55.2	81.2	883	8	AG739605 HS_5381_B
86	54.8	80.6	263	8	AG266169 CITR1-E1-
87	54.8	80.6	397	8	AG166346 HS_3124_B
88	54.8	80.6	580	8	AG628359 CITR1-E1-
89	54.8	80.6	684	8	AG112508 RPT1-11-10
90	54.4	80.0	262	8	AG096680 HS_3032_B
91	53.8	79.1	372	9	AG266378 Homo sapi
92	53.8	79.1	547	8	AG139345 HS_3082_A
93	53.6	78.8	135	8	AG347084 RPT1-11-11
94	53.6	78.8	270	8	AG046487 RPT1-11-3
95	53.6	78.8	355	8	AG540409 RPT1-11-3
96	53.6	78.8	423	3	AG362220 HS_5049_B
97	53.6	78.8	446	4	BF948124 CM0-NN115

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 44.3008 Seconds  
(without alignments)  
9130.760 Million cell updates/sec

Title: US-09-854-867-3

Perfect score: 68  
Sequence: 1 gacacagtcagagatgctc.....aagagttacatcacctcgggt 68

Scoring table:  
IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

Published Applications NA:\*

1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/prodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*  
9: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
10: /cgn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
11: /cgn2\_6/prodata/1/pubpna/US09C\_NEW\_PUB.seq:\*  
12: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/prodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/prodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	68	10	US-09-854-867-3
2	61.6	90.6	473	9	US-09-864-761-2422
3	60	88.2	467	13	US-10-027-632-319355
4	60	88.2	467	17	US-10-027-632-319355
5	60	88.2	593	13	US-10-027-632-3521
6	60	88.2	593	17	US-10-027-632-3521
7	60	88.2	630	13	US-10-027-632-1917
8	60	88.2	630	13	US-10-027-632-1918
9	60	88.2	630	17	US-10-027-632-1917
10	60	88.2	630	17	US-10-027-632-1918
11	60	88.2	672	13	US-10-027-632-113100

12	60	88.2	672	13	US-10-027-632-113101	Sequence 113101.
13	60	88.2	672	13	US-10-027-632-113102	Sequence 113102.
14	60	88.2	672	17	US-10-027-632-113100	Sequence 113100.
15	60	88.2	672	17	US-10-027-632-113101	Sequence 113101.
16	60	88.2	672	17	US-10-027-632-113102	Sequence 113102.
17	59	86.8	506	9	US-09-864-761-13029	Sequence 13029, A
18	58.4	85.9	657	13	US-10-027-632-315903	Sequence 315903.
19	58.4	85.9	657	17	US-10-027-632-315903	Sequence 315903.
20	56.8	83.5	530	10	US-09-814-353-2271	Sequence 2271, Ap
21	56.8	83.5	530	10	US-09-814-353-8611	Sequence 8611, Ap
22	56.8	83.5	574	10	US-09-814-353-14995	Sequence 14995, A
23	55.2	81.2	499	9	US-09-783-590-4181	Sequence 4181, Ap
24	55.2	81.2	858	13	US-10-027-632-173562	Sequence 173562.
25	55.2	81.2	858	13	US-10-027-632-173563	Sequence 173563.
26	55.2	81.2	858	17	US-10-027-632-173562	Sequence 173562.
27	55.2	81.2	858	17	US-10-027-632-173563	Sequence 173563.
28	52	76.5	184	9	US-09-738-973-536	Sequence 536, App
29	52	76.5	184	9	US-09-854-133-536	Sequence 536, App
30	52	76.5	184	15	US-10-144-649A-536	Sequence 536, App
31	52	76.5	625	13	US-10-027-632-3250	Sequence 3250, Ap
32	52	76.5	625	13	US-10-027-632-3251	Sequence 3251, Ap
33	52	76.5	625	17	US-10-027-632-3250	Sequence 3250, Ap
34	52	76.5	625	17	US-10-027-632-3251	Sequence 3251, Ap
35	51.6	75.9	605	13	US-10-027-632-95155	Sequence 95155, A
36	51.6	75.9	605	13	US-10-027-632-318612	Sequence 318612.
37	51.6	75.9	605	17	US-10-027-632-95155	Sequence 95155, A
38	51.6	75.9	605	17	US-10-027-632-318612	Sequence 318612.
39	50.4	74.1	1040	13	US-10-027-632-2571	Sequence 2571, Ap
40	50.4	74.1	1040	13	US-10-027-632-2572	Sequence 2572, Ap
41	50.4	74.1	1040	13	US-10-027-632-2573	Sequence 2573, Ap
42	50.4	74.1	1040	13	US-10-027-632-2574	Sequence 2574, Ap
43	50.4	74.1	1040	17	US-10-027-632-2571	Sequence 2571, Ap
44	50.4	74.1	1040	17	US-10-027-632-2572	Sequence 2572, Ap
45	50.4	74.1	1040	17	US-10-027-632-2573	Sequence 2573, Ap
46	50.4	74.1	1040	17	US-10-027-632-2574	Sequence 2574, Ap
47	50	73.5	758	13	US-10-027-632-4438	Sequence 4438, Ap
48	50	73.5	758	17	US-10-027-632-4438	Sequence 4438, Ap
49	49	72.1	190	9	US-09-864-761-29592	Sequence 29592, A
50	48.8	71.8	693	13	US-10-027-632-17960	Sequence 17960, A
51	48.8	71.8	693	13	US-10-027-632-17961	Sequence 17961, A
52	48.8	71.8	693	13	US-10-027-632-17962	Sequence 17962, A
53	48.8	71.8	693	17	US-10-027-632-17960	Sequence 17960, A
54	48.8	71.8	693	17	US-10-027-632-17961	Sequence 17961, A
55	48.8	71.8	693	17	US-10-027-632-17962	Sequence 17962, A
56	48	70.6	617	13	US-10-027-632-6018	Sequence 6018, Ap
57	48	70.6	617	13	US-10-027-632-6019	Sequence 6019, Ap
58	48	70.6	617	13	US-10-027-632-6020	Sequence 6020, Ap
59	48	70.6	617	13	US-10-027-632-6021	Sequence 6021, Ap
60	48	70.6	617	17	US-10-027-632-6018	Sequence 6018, Ap
61	48	70.6	617	17	US-10-027-632-6019	Sequence 6019, Ap
62	48	70.6	617	17	US-10-027-632-6020	Sequence 6020, Ap
63	48	70.6	617	17	US-10-027-632-6021	Sequence 6021, Ap
64	45.8	67.4	590	13	US-10-027-632-311425	Sequence 311425.
65	45.8	67.4	590	17	US-10-027-632-311425	Sequence 311425.
66	44.2	65.0	201	9	US-09-864-761-19153	Sequence 19153, A
67	44.2	65.0	220	9	US-09-783-590-4004	Sequence 4004, Ap
68	38	55.9	209	17	US-10-242-535A-9959	Sequence 9959, Ap
69	38	55.9	209	17	US-10-085-783A-9959	Sequence 9959, Ap
70	32.2	47.4	568	13	US-10-027-632-228175	Sequence 228175.
71	32.2	47.4	568	17	US-10-027-632-228175	Sequence 228175.
72	31	45.6	1104	13	US-10-027-632-208393	Sequence 208393.
73	31	45.6	1104	17	US-10-027-632-208393	Sequence 208393.
74	30.6	45.0	703	13	US-10-027-632-113092	Sequence 113092.
75	29.6	43.5	400	17	US-10-027-632-113092	Sequence 113092.
76	29.6	43.5	400	17	US-10-085-783A-9545	Sequence 9545, Ap
77	29.6	43.5	400	17	US-10-085-783A-9545	Sequence 9545, Ap
78	29.6	43.5	635	13	US-10-027-632-113090	Sequence 113090.
79	29.6	43.5	635	13	US-10-027-632-113091	Sequence 113091.
80	29.6	43.5	635	17	US-10-027-632-113090	Sequence 113090.
81	29.6	43.5	635	17	US-10-027-632-113091	Sequence 113091.
82	29.4	43.2	370	13	US-10-027-632-271462	Sequence 271462.
83	29.4	43.2	370	17	US-10-027-632-271462	Sequence 271462.
84	29.4	43.2	608	13	US-10-027-632-202596	Sequence 202596.



OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 12.3906 Seconds  
(without alignments)

8979.909 Million cell updates/sec

Title: US-09-854-867-3

Perfect score: 68

Sequence: 1 gatcagctgagagatagtc.....aagagttacacactggt 68

Scoring table:

IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents NA: \*  
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2: /cgn2\_6/prodata/1/ina/5B.COMB.seq.\*  
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5: /cgn2\_6/prodata/1/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	68	US-09-573-080A-3	Sequence 3, Appl
2	52	76.5	184	US-09-854-133-536	Sequence 53, App
3	44.2	65.0	356	US-09-513-999C-13463	Sequence 13463, A
4	32.8	48.2	156942	US-09-949-016-12227	Sequence 12227, A
5	32.8	48.2	156950	US-09-949-016-15946	Sequence 15946, A
6	29	42.6	601	US-09-949-016-149536	Sequence 149536, A
7	29	42.6	601	US-09-949-016-149537	Sequence 149537, A
8	29	42.6	601	US-09-949-016-149597	Sequence 149597, A
9	29	42.6	156942	US-09-949-016-12227	Sequence 12227, A
10	29	42.6	156950	US-09-949-016-15946	Sequence 15946, A
11	28	41.2	56939	US-09-949-016-13613	Sequence 13613, A
12	28	41.2	76281	US-09-949-016-12708	Sequence 12708, A
13	26	38.2	601	US-09-949-016-149602	Sequence 149602, A
14	25.6	37.6	294	US-09-411-977-10	Sequence 10, Appl
15	25.6	37.6	294	US-10-057-951-10	Sequence 10, Appl
16	25.6	37.6	50109	US-09-949-016-14112	Sequence 14112, A
17	25.6	37.6	470	US-09-621-976-10621	Sequence 10621, A
18	25	36.8	1149	US-09-280-116-196	Sequence 196, App
19	25	36.8	2231	US-09-008-271A-24	Sequence 24, Appl
20	25	36.8	152481	US-09-949-016-12521	Sequence 12521, A
21	25	36.8	152798	US-09-949-016-12775	Sequence 12775, A
22	25	36.8	152822	US-09-949-016-17518	Sequence 17518, A
23	25	36.8	152822	US-09-949-016-17519	Sequence 17519, A
24	24.8	36.5	168174	US-10-071-411A-63	Sequence 63, Appl
25	24.8	36.5	168273	US-10-071-411A-2	Sequence 2, Appl
26	24.6	36.2	2418	US-09-245-808-2	Sequence 2, Appl
27	24.6	36.2	31573	US-09-949-016-16327	Sequence 16327, A

C	28	24.4	35.9	601	4	US-09-949-016-149541	Sequence 149541, A
C	29	24.4	35.9	601	4	US-09-949-016-149598	Sequence 149598, A
C	30	24.2	35.6	478	4	US-09-621-976-1639	Sequence 1639, Ap
C	31	24	35.3	601	4	US-09-949-016-149544	Sequence 149544, A
C	32	24	35.3	601	4	US-09-949-016-149545	Sequence 149545, A
C	33	23.8	35.0	497	4	US-09-621-976-15952	Sequence 15952, Ap
C	34	23.8	35.0	601	4	US-09-949-016-65952	Sequence 65952, A
C	35	23.8	35.0	601	4	US-09-949-016-182062	Sequence 182062, A
C	36	23.8	35.0	601	4	US-09-949-016-182290	Sequence 182290, A
C	37	23.8	35.0	1316	4	US-08-956-171E-111	Sequence 111, App
C	38	23.8	35.0	1316	4	US-08-781-986A-111	Sequence 111, App
C	39	23.8	35.0	3222	3	US-08-936-165A-111	Sequence 111, App
C	40	23.8	35.0	12449	4	US-09-949-016-15755	Sequence 15755, A
C	41	23.8	35.0	31300	4	US-09-949-016-15967	Sequence 15967, A
C	42	23.8	35.0	235452	4	US-09-949-016-16755	Sequence 16755, A
C	43	23.4	34.4	26049	4	US-09-949-016-16224	Sequence 16224, A
C	44	23.2	34.1	145928	4	US-09-949-016-15444	Sequence 15444, A
C	45	23.2	34.1	1664976	4	US-08-916-471B-1	Sequence 1, Appl
C	46	23.2	34.1	1664976	4	US-09-692-570-1	Sequence 1, Appl
C	47	23	33.8	601	4	US-09-949-016-70935	Sequence 70935, A
C	48	23	33.8	601	4	US-09-949-016-164502	Sequence 164502, A
C	49	23	33.8	795	4	US-09-134-000C-3304	Sequence 3304, Ap
C	50	23	33.8	856	3	US-09-171-517B-15	Sequence 15, Appl
C	51	23	33.8	2256	4	US-09-252-991A-16099	Sequence 16099, A
C	52	23	33.8	6688	4	US-09-252-991A-16502	Sequence 16502, A
C	53	23	33.8	12241	4	US-09-813-451B-12	Sequence 12, Appl
C	54	23	33.8	13737	3	US-09-538-414-10	Sequence 4, Appl
C	55	23	33.8	13737	3	US-10-074-279-10	Sequence 10, Appl
C	56	23	33.8	13737	3	US-10-074-279-10	Sequence 10, Appl
C	57	23	33.8	14446	4	US-09-810-861B-4	Sequence 4, Appl
C	58	23	33.8	190078	4	US-09-949-016-1707	Sequence 12707, A
C	59	23	33.8	190078	4	US-09-949-016-17026	Sequence 17026, A
C	60	23	33.8	276687	4	US-09-949-016-1840	Sequence 13840, A
C	61	22.8	33.5	78157	4	US-09-949-016-16466	Sequence 16466, A
C	62	22.8	33.5	78157	4	US-09-949-016-16467	Sequence 16467, A
C	63	22.6	33.2	1372	4	US-09-976-594-869	Sequence 869, App
C	64	22.6	33.2	37269	4	US-09-949-016-16672	Sequence 16672, A
C	65	22.6	33.2	45249	4	US-09-949-016-13228	Sequence 13228, A
C	66	22.6	33.2	87774	4	US-09-949-016-1821	Sequence 1821, A
C	67	22.6	33.2	238815	4	US-09-949-016-16274	Sequence 16274, A
C	68	22.4	32.9	601	4	US-09-949-016-57396	Sequence 57396, A
C	69	22.4	32.9	1925	4	US-09-620-312D-488	Sequence 488, App
C	70	22.4	32.9	3220	4	US-09-949-016-991	Sequence 981, App
C	71	22.4	32.9	49378	4	US-09-949-016-13408	Sequence 13408, A
C	72	22.4	32.9	268449	4	US-09-949-016-17244	Sequence 17244, A
C	73	22.4	32.9	1230025	4	US-09-198-452A-1	Sequence 1, Appl
C	74	22.4	32.9	1230230	4	US-09-438-185A-1	Sequence 1, Appl
C	75	22.2	32.6	601	4	US-09-949-016-139932	Sequence 139932, A
C	76	22.2	32.6	607	3	US-09-105-390-10	Sequence 10, Appl
C	77	22.2	32.6	1349	3	US-09-105-390-2	Sequence 2, Appl
C	78	22.2	32.6	3336	4	US-09-949-016-4510	Sequence 4510, Ap
C	79	22.2	32.6	4843	3	US-08-986-485-1	Sequence 1, Appl
C	80	22.2	32.6	25401	4	US-09-949-016-13345	Sequence 13345, A
C	81	22.2	32.6	50062	4	US-09-949-016-13809	Sequence 13809, A
C	82	22.2	32.6	118067	4	US-09-497-855A-32	Sequence 32, Appl
C	83	22.2	32.6	145812	4	US-09-949-016-15698	Sequence 15698, A
C	84	22.2	32.6	157032	4	US-09-949-016-15502	Sequence 15502, A
C	85	22	32.4	2100	4	US-10-061-942A-9	Sequence 9, Appl
C	86	22	32.4	25122	4	US-09-949-016-13132	Sequence 16132, A
C	87	22	32.4	109159	4	US-09-949-016-14169	Sequence 14169, A
C	88	22	32.4	109159	4	US-09-949-016-14170	Sequence 14170, A
C	89	21.8	32.1	323	4	US-09-621-976-2180	Sequence 2180, Ap
C	90	21.8	32.1	2777	4	US-09-949-016-1227	Sequence 1227, Ap
C	91	21.8	32.1	2823	4	US-09-704-611-4	Sequence 4, Appl
C	92	21.8	32.1	2892	4	US-09-704-611-3	Sequence 3, Appl
C	93	21.8	32.1	24979	2	US-08-147-777-3	Sequence 3, Appl
C	94	21.8	32.1	24979	2	US-08-452-877-3	Sequence 3, Appl
C	95	21.8	32.1	24979	5	PCT-US93-03985-3	Sequence 3, Appl
C	96	21.8	32.1	36148	4	US-09-949-016-12969	Sequence 12969, A
C	97	21.8	32.1	94156	4	US-09-949-016-12388	Sequence 12388, A
C	98	21.8	32.1	102406	4	US-09-949-016-14673	Sequence 14673, A
C	99	21.8	32.1	1830121	4	US-09-557-884-1	Sequence 1, Appl
C	100	21.8	32.1	1830121	4	US-09-643-990A-1	Sequence 1, Appl

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:44:41 ; Search time 40.8212 Seconds  
(without alignments)  
9861.108 Million cell updates/sec

Title: US-09-854-867-3  
Perfect score: 68  
Sequence: 1 gatcagtcgacagatagtc.....aagatracatcacctgggt 68

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N\_Geneseq\_16Dec04:.\*  
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6: geneseq2002as:.\*  
7: geneseq2002bs:.\*  
8: geneseq2003as:.\*  
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12: geneseq2004as:.\*  
13: geneseq2004bs:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	68	7	AD30970 Human gen
2	61.6	90.6	473	4	AA112501 Probe #24
3	61.6	90.6	473	4	ABA54205 Human foe
4	61.6	90.6	473	4	ABA23956 Probe #24
5	61.6	90.6	473	4	AAK02483 Human bra
6	61.6	90.6	473	6	ABS02375 Human gen
7	59	86.8	506	4	AA141915 Probe #10
8	59	86.8	506	4	AAK10298 Human bra
9	58.4	85.9	134	10	ADP38189 Synchro
10	56.8	83.5	530	5	AD175869 Human ova
11	56.8	83.5	530	5	AD175869 Human ova
12	56.8	83.5	574	5	AD141105 Human ova
13	55.2	81.2	191	10	ADP38204 Synchro
14	55.2	81.2	250	10	ACD96972 Human col
15	52	76.5	184	4	AAAD3556 Human lun
16	52	76.5	184	10	ADDE6844 Human lun
17	52	76.5	184	10	ADDE6844 Human lun
18	49	72.1	190	4	AA154950 Probe #23
19	49	72.1	190	4	AAK22946 Human bra
20	48.8	71.8	305	3	AAAS7082 Human col

21	48.8	71.8	305	6	ABT12504
22	48.8	71.8	305	10	ACD91798
23	46	67.6	294	10	ACD97075
24	44.2	65.0	201	4	AA121692
25	44.2	65.0	201	4	ABA66769
26	44.2	65.0	201	4	ABA33833
27	44.2	65.0	201	4	AAK15201
28	44.2	65.0	201	6	AB14880 Human gen
29	44.2	65.0	356	3	ACD93882
30	34.2	50.3	166	10	ACD93882
31	33	48.5	165199	6	ABK83460
32	32.8	48.2	849	4	AAH06738
33	31.4	46.2	117	3	AAAS7076
34	31.4	46.2	117	6	ABT12498
35	31.4	46.2	117	10	ACD91792
36	30.6	45.0	300	2	AA124352
37	28.4	41.8	284	4	AA106830
38	28.4	41.8	3003	12	ADN06033
39	28.4	41.8	3083	4	AA106831
40	28.4	41.8	4132	11	ACN91983
41	28.4	41.8	8191	4	ABK43033
42	28.4	41.8	8191	4	AA106832
43	28.4	41.8	8191	9	ADBE1189
44	28	41.2	1989	10	ADAS3544
45	28	41.2	2653	10	ADAS3601
46	28	41.2	4418	4	ABK43031
47	28	41.2	4418	9	ADBE1187
48	28	41.2	4418	9	ADBE1188
49	28	41.2	4418	4	AAK80928
50	27.6	40.6	648	4	AAK80928
51	27.6	40.6	165199	6	ABK83460
52	27	39.7	3144	11	ADN03175
53	26.8	39.4	544	12	ADN12721
54	26.8	39.4	544	12	ADN12721
55	26.6	39.1	481	4	AA113802
56	26.6	39.1	481	4	AA135162
57	26.6	39.1	481	4	AB28826
58	26.6	39.1	481	5	AA103676
59	26.4	38.8	523	12	ADN12651
60	26.4	38.8	532	12	ADN12817
61	26.4	38.8	798	12	ADN13802
62	26.4	38.8	2213	10	ADAS3461
63	26.4	38.8	2654	10	ADDE5426
64	26.4	38.8	4369	12	AD063952
65	26	38.2	485	4	AAK61675
66	26	38.2	2114	4	AAH16027
67	25.8	37.9	521	5	AD172251
68	25.8	37.9	521	5	AD172251
69	25.8	37.9	545	6	ABQ56343
70	25.8	37.9	619	5	ADL43780
71	25.6	37.6	291	2	AAV99643
72	25.6	37.6	294	4	AD03468
73	25.6	37.6	340	4	AAE92291
74	25.6	37.6	100543	6	ABE52816
75	25.6	37.6	128978	6	ABK83459
76	25.6	37.6	128978	8	AAAS4587
77	25.6	37.6	128978	13	ADDE5294
78	25.4	37.4	16273	4	AAK80688
79	25.4	37.4	16273	4	AAK79625
80	25	36.8	230	10	ADD26739
81	25	36.8	429	4	AAH09222
82	25	36.8	521	2	AAV89955
83	25	36.8	521	9	ACH35570
84	25	36.8	537	12	ACH71365
85	25	36.8	598	6	ABK35701
86	25	36.8	748	6	ABK35158
87	25	36.8	798	4	AAH07861
88	25	36.8	1149	6	ABK30426
89	25	36.8	1340	6	AACT3307
90	25	36.8	1345	6	ABQ54369
91	25	36.8	1485	5	AAE79250
92	25	36.8	1485	5	AAE64441
93	25	36.8	1485	5	AAE64441

AB112504	Orestes s
ACD91798	Human col
ACD97075	Human col
AA121692	Probe #11
ABA66769	Human foe
ABA33833	Probe #12
AAK15201	Human bra
AB14880	Human gen
ACD93882	Human sec
ABK83460	Human col
AAH06738	Human col
AAAS7076	Human col
ABT12498	Orestes s
ACD91792	Human col
AA124352	Human gen
AA106830	Human rep
ADN06033	Antipso
AA106831	Human rep
ACN91983	Breast ca
ABK43033	Genomic s
AA106832	Human rep
ADBE1189	Connectiv
ADAS3544	Human cod
ADAS3601	Human cod
ABK43032	Genomic s
ADBE1187	Connectiv
ADBE1188	Connectiv
AAK80928	Human imm
ABK83460	Human CDN
ADN03175	Human CDN
ADN12721	Human pro
AD172251	Human pro
AD172251	Human pro
AD13802	Human pro
ADAS3461	Human cod
ADDE5426	Human gen
AD063952	Novel hum
AAK61675	Human imm
AAH16027	Human CDN
AD172251	Human ova
AD13736	Human ova
ABQ56343	Human col
ADL43780	Human ova
AAV99643	Human t-p
AD03468	Human t-p
AAE92291	Bovine ma
ABE52816	Genomic D
ABK83459	Human CDN
AAAS4587	Human LIM
ADDE5294	Dryg ther
AAK80688	Human imm
AAK79625	Human imm
ADD26739	Human adi
AAH09222	Human CDN
AAV89955	EST clone
ACH35570	Human end
ACH71365	Human gen
ABK35701	CDNA seg
ABK35158	Human CDN
AAH07861	Human CDN
ABK30426	Human G-P
AACT3307	Human sec
ABQ54369	Human ova
AAE79250	DNA encod
AAE64441	DNA encod
AAE64441	DNA encod

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 / Search time 311.93 Seconds  
(without alignment)  
10563.118 Million cell updates/sec

Title: US-09-854-867-3

Perfect score: 68

Sequence: 1 gacacgtgcagacatgctc.....aagagttacatcactggtggt 68

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database:

1: gb\_da:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_ro:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66.4	97.6	144432	2	AF276983 Homo sapi
2	66.4	97.6	163399	2	AC079860 Homo sapi
3	66.4	97.6	186759	9	AL645608 Homo sapi
4	66.4	97.6	200491	2	AB107102 Homo sapi
5	66.4	97.6	327883	2	BX571684 Homo sapi
6	64.8	95.3	38986	9	AY546236 Homo sapi
7	64.8	95.3	104026	9	BS000579 Homo sapi
8	64.8	95.3	142000	2	AC141241 Homo sapi
9	64.8	95.3	152654	2	AC141882 Homo sapi
10	64.8	95.3	170856	2	AC068160 Homo sapi
11	64.8	95.3	175868	2	AC147660 Homo sapi
12	64.8	95.3	179403	2	AC146250 Homo sapi
13	64.8	95.3	179013	9	AC022370 Homo sapi
14	64.8	95.3	181432	9	BX649480 Homo sapi
15	64.8	95.3	238079	9	AC147656 Homo sapi
16	63.8	93.8	172294	9	BX546479 Homo sapi
17	63.2	92.9	345	9	AY546202 Homo sapi
18	63.2	92.9	346	9	AY546211 Homo sapi
19	63.2	92.9	346	9	AY546211 Homo sapi

20	63.2	92.9	416	9	AY546215 Homo sapi
21	63.2	92.9	639	9	AF282526 Homo sapi
22	63.2	92.9	1445	9	AF270544 Homo sapi
23	63.2	92.9	29891	9	AP006330 Homo sapi
24	63.2	92.9	31503	9	AP006328 Homo sapi
25	63.2	92.9	36971	9	AL732375 Homo sapi
26	63.2	92.9	39002	9	AL845259 Homo sapi
27	63.2	92.9	56731	2	AC087706 Homo sapi
28	63.2	92.9	104154	2	AC004902 Homo sapi
29	63.2	92.9	110773	2	BX005259 Homo sapi
30	63.2	92.9	126625	9	AY028079 Homo sapi
31	63.2	92.9	137001	9	AP001005 Homo sapi
32	63.2	92.9	142000	2	AC141241 Homo sapi
33	63.2	92.9	157606	2	AC069172 Homo sapi
34	63.2	92.9	168066	2	AC052236 Homo sapi
35	63.2	92.9	170856	2	AC068160 Homo sapi
36	63.2	92.9	179013	9	AC022370 Homo sapi
37	63.2	92.9	181432	9	BX649480 Homo sapi
38	63.2	92.9	194917	2	AC069343 Homo sapi
39	63.2	92.9	194917	2	AC069343 Homo sapi
40	63.2	92.9	211173	9	AL671532 Homo sapi
41	63.2	92.9	220206	2	AC140726 Homo sapi
42	63.2	92.9	220897	2	AL954635 Homo sapi
43	61.6	90.6	72	9	HUMRSSAUH
44	61.6	90.6	345	9	AY546206 Homo sapi
45	61.6	90.6	347	9	AY546197 Homo sapi
46	61.6	90.6	361	9	AY546237 Homo sapi
47	61.6	90.6	361	9	AY546242 Homo sapi
48	61.6	90.6	394	9	HUMRSSAUH
49	61.6	90.6	473	6	C0066634 Sequence
50	61.6	90.6	473	6	C0171026 Sequence
51	61.6	90.6	473	6	C0254249 Sequence
52	61.6	90.6	473	6	C0291261 Sequence
53	61.6	90.6	473	6	C0328380 Sequence
54	61.6	90.6	615	9	AY546195 Homo sapi
55	61.6	90.6	635	9	AF282527 Homo sapi
56	61.6	90.6	3664	9	HSU74497 Homo sapi
57	61.6	90.6	133461	2	AC025968 Homo sapi
58	61.6	90.6	162209	2	AC020702 Homo sapi
59	61.6	90.6	172294	9	BX546479 Homo sapi
60	61.6	90.6	182649	2	AC023033 Homo sapi
61	61.6	90.6	183303	9	AC064866 Homo sapi
62	61.6	90.6	183495	9	AC129664 Homo sapi
63	61.6	90.6	189853	2	AC130423 Homo sapi
64	61.6	90.6	193867	2	AC022179 Homo sapi
65	61.6	90.6	211173	9	AL671532 Homo sapi
66	61.6	90.6	296385	2	BX548253 Homo sapi
67	60.6	89.1	167135	9	AC137488 Homo sapi
68	60.6	88.2	72	9	HUMRSSAUH
69	60.6	88.2	345	9	AY546219 Homo sapi
70	60.6	88.2	345	9	AY546223 Homo sapi
71	60.6	88.2	345	9	AY546227 Homo sapi
72	60.6	88.2	345	9	AY546231 Homo sapi
73	60.6	88.2	361	9	AY546241 Homo sapi
74	60.6	88.2	429	9	AY546238 Homo sapi
75	60.6	88.2	429	9	AY546240 Homo sapi
76	60.6	88.2	429	9	AY546243 Homo sapi
77	60.6	88.2	429	9	AY546244 Homo sapi
78	60.6	88.2	897	9	AF283053 Homo sapi
79	60.6	88.2	901	9	AF283054 Homo sapi
80	60.6	88.2	901	9	AF283055 Homo sapi
81	60.6	88.2	1656	9	AF270545 Homo sapi
82	60.6	88.2	65276	2	AC084190 Homo sapi
83	60.6	88.2	162209	2	AC020702 Homo sapi
84	60.6	88.2	186051	2	BX005324 Homo sapi
85	60.6	88.2	189610	2	AC104301 Homo sapi
86	60.6	88.2	189653	2	AC130423 Homo sapi
87	60.6	88.2	193867	2	AC022179 Homo sapi
88	59.8	86.8	506	6	C0101742 Sequence
89	59.8	86.8	506	6	C0336195 Sequence
90	58.4	85.9	134	6	AX927327 Sequence
91	58.4	85.9	134	8	AJ718176 Nicotiana
92	58.4	85.9	429	9	AY546245 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:09:22 ; Search time 1101.05 Seconds  
(without alignments)  
10025.556 Million cell updates/sec

Title: US-09-854-867-2  
Perfect score: 290  
Sequence: 1 ggcgcggcgccggtgctcac.....agacccctgcctcaaaaaa 290

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	243.6	84.0	342	5	BX484854 DKFZP686L
C 2	243.6	84.0	409	7	CN276487
C 3	243.6	84.0	1686	3	CR619941
C 4	243.6	84.0	1755	3	CR609780 full-length
C 5	242	83.4	368	4	BG059314 nah48c05
C 6	242	83.4	424	8	AQ113643 CIR-HSP-2
C 7	240.4	82.9	352	2	BF804385
C 8	240.4	82.9	521	2	AM970571
C 9	240.4	82.9	990	4	BM803650
C 10	238.8	82.3	423	5	BM991096
C 11	238.8	82.3	447	5	BX489032
C 12	238.8	82.3	454	1	AI634187
C 13	238.8	82.3	514	8	B81985
C 14	238.8	82.3	514	1	AI754653
C 15	238.8	82.3	832	4	BG697217
C 16	238.8	82.3	907	4	BG547933
C 17	238.8	82.3	361	8	AQ037231
C 18	237.8	82.0	337	5	BUS66980
C 19	237.8	82.0	333	2	BF805088
C 20	237.8	82.0	439	1	AV738383
C 21	237.8	82.0	474	1	AI457313
C 22	237.8	82.0	490	8	AQ426532
C 23	237.8	82.0	575	8	AQ587429
C 24	237.8	82.0	676	9	AG178621

Result No.	Score	Query Match	Length	ID	Description
C 1	243.6	84.0	342	5	BX484854 DKFZP686L
C 2	243.6	84.0	409	7	CN276487
C 3	243.6	84.0	1686	3	CR619941
C 4	243.6	84.0	1755	3	CR609780 full-length
C 5	242	83.4	368	4	BG059314 nah48c05
C 6	242	83.4	424	8	AQ113643 CIR-HSP-2
C 7	240.4	82.9	352	2	BF804385
C 8	240.4	82.9	521	2	AM970571
C 9	240.4	82.9	990	4	BM803650
C 10	238.8	82.3	423	5	BM991096
C 11	238.8	82.3	447	5	BX489032
C 12	238.8	82.3	454	1	AI634187
C 13	238.8	82.3	514	8	B81985
C 14	238.8	82.3	514	1	AI754653
C 15	238.8	82.3	832	4	BG697217
C 16	238.8	82.3	907	4	BG547933
C 17	238.8	82.3	361	8	AQ037231
C 18	237.8	82.0	337	5	BUS66980
C 19	237.8	82.0	333	2	BF805088
C 20	237.8	82.0	439	1	AV738383
C 21	237.8	82.0	474	1	AI457313
C 22	237.8	82.0	490	8	AQ426532
C 23	237.8	82.0	575	8	AQ587429
C 24	237.8	82.0	676	9	AG178621

C 25	237.4	81.9	521	5	BU617227
C 26	237.4	81.9	580	5	BO053726
C 27	237.4	81.9	598	5	BO017808
C 28	237.4	81.9	616	5	BU617236
C 29	237.4	81.9	731	1	AI687343
C 30	237.2	81.8	372	8	AQ163866
C 31	237.2	81.8	390	5	BUS88888
C 32	237.2	81.8	438	7	CR739570
C 33	237.2	81.8	461	1	AA225406
C 34	237.2	81.8	466	2	AM722294
C 35	237.2	81.8	486	2	AM958862
C 36	237.2	81.8	523	8	AQ480399
C 37	237.2	81.8	589	6	CA439973
C 38	237.2	81.8	590	8	AQ421062
C 39	237.2	81.8	615	5	BU783874
C 40	237.2	81.8	646	1	AL134940
C 41	237.2	81.8	705	5	BU616173
C 42	237.2	81.8	731	7	CN307840
C 43	237.2	81.8	745	9	AG015273
C 44	237.2	81.8	750	9	AG015272
C 45	237.2	81.8	866	8	B2771933
C 46	237.2	81.7	960	6	CD245816
C 47	237.2	81.7	857	5	BU570414
C 48	236.2	81.4	539	8	AQ379787
C 49	236.2	81.4	556	5	BM997889
C 50	236.2	81.4	666	5	BU616112
C 51	236.2	81.4	763	1	AU130337
C 52	236.2	81.4	950	6	CD558421
C 53	235.8	81.3	563	1	AU144540
C 54	235.6	81.2	380	1	AA613624
C 55	235.6	81.2	388	2	AM069227
C 56	235.6	81.2	458	1	AT733856
C 57	235.6	81.2	480	1	AL1635028
C 58	235.6	81.2	482	5	BU735500
C 59	235.6	81.2	582	1	AI923451
C 60	235.6	81.2	583	1	BP872816
C 61	235.6	81.2	602	6	CD369014
C 62	235.6	81.2	677	4	BI858435
C 63	235.6	81.2	678	8	AQ387027
C 64	235.6	81.2	697	9	AG010078
C 65	235.6	81.2	714	9	AG009651
C 66	235.6	81.2	735	7	CF146929
C 67	235.6	81.2	1111	4	BM466902
C 68	235.6	81.2	1555	3	BC022315
C 69	235.6	81.2	1820	3	AF318360
C 70	235.6	81.2	5404	3	HSW804865
C 71	235.6	81.2	5535	3	CR749478
C 72	235.2	81.1	486	1	AI601229
C 73	235.2	81.1	967	8	AQ744206
C 74	235.2	81.1	333	5	BU540252
C 75	234.8	81.0	472	5	BM983330
C 76	234.8	81.0	1100	4	BM802793
C 77	234.6	80.9	319	5	BU655560
C 78	234.6	80.9	441	1	AA441810
C 79	234.6	80.9	546	4	BM697526
C 80	234.6	80.9	567	1	AV761107
C 81	234.6	80.9	611	6	CD704731
C 82	234.6	80.9	698	7	CF146894
C 83	234.6	80.9	713	6	CA308268
C 84	234.4	80.8	360	8	B91708
C 85	234.2	80.8	338	1	AV760915
C 86	234.2	80.8	560	1	CD238756
C 87	234.2	80.7	327	1	AA483606
C 88	234	80.7	337	3	AA570740
C 89	234	80.7	393	6	CA434441
C 90	234	80.7	421	8	B76341
C 91	234	80.7	433	2	AM105346
C 92	234	80.7	451	1	AV695478
C 93	234	80.7	455	1	AA504211
C 94	234	80.7	509	2	BF916871
C 95	234	80.7	511	1	AV760508
C 96	234	80.7	568	6	CD517289
C 97	234	80.7			

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 188.93 Seconds

(without alignments)  
9130.760 Million cell updates/sec

Title: US-09-854-867-2

Perfect score: 290

Sequence: 1 ggcgcggcggtgcacac.....agaccctctcaaaaaa 290

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: Published Applications NA:\*  
2: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US05\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US04\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US03\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US02\_PUBCOMB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US01\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US00\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US05\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US04\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US03\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US02\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US01\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US00\_PUBCOMB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	290	100.0	US-09-854-867-2	Sequence 2, Appl1
2	284.8	98.2	US-10-115-378-1	Sequence 1, Appl1
3	284.8	98.2	US-10-762-966-1	Sequence 1, Appl1
4	259.2	89.4	US-10-115-278-2	Sequence 2, Appl1
5	259.2	89.4	US-10-762-966-2	Sequence 2, Appl1
6	253.8	87.5	US-10-255-434-1	Sequence 1, Appl1
7	251	86.6	US-10-394-485-26	Sequence 26, Appl1
8	248.6	85.7	US-09-964-824A-509	Sequence 509, App
9	248.6	85.7	US-09-963-347-1	Sequence 1, Appl1
10	247.4	85.3	US-10-255-434-2	Sequence 2, Appl1
11	246.8	85.1	US-10-017-161-2415	Sequence 2415, App

12	246.8	85.1	21925	17	US-10-292-798-2055	Sequence 2055, App
13	245.2	84.6	46215	19	US-10-741-600-17973	Sequence 17973, A
14	243.6	84.0	60940	17	US-10-052-482-88	Sequence 88, Appl1
15	243.4	83.9	289	14	US-10-115-278-3	Sequence 3, Appl1
16	243.4	83.9	289	18	US-10-762-966-3	Sequence 966, A
17	241.6	83.3	670	13	US-10-027-632-99522	Sequence 99522, A
18	241.6	83.3	670	13	US-10-027-632-99522	Sequence 99522, A
19	241.6	83.3	670	17	US-10-027-632-99522	Sequence 99523, A
20	241.6	83.3	670	17	US-10-027-632-99523	Sequence 99523, A
21	241.4	83.2	98716	19	US-10-741-600-17754	Sequence 17754, A
22	241	83.1	15577	14	US-10-158-160A-8	Sequence 8, Appl1
23	241	83.1	32367	14	US-10-158-160A-14	Sequence 14, Appl1
24	241	83.1	35236	13	US-10-087-192-370	Sequence 370, App
25	241	83.1	59554	17	US-10-052-482-202	Sequence 202, App
26	240.8	83.0	288	16	US-10-229-058B-14	Sequence 14, Appl1
27	240.6	83.0	26184	15	US-10-017-161-2043	Sequence 2043, App
28	240.6	83.0	26184	17	US-10-027-798-1689	Sequence 1689, App
29	240.4	82.9	2490	13	US-10-027-632-102144	Sequence 102144, Sequence 111607,
30	240.4	82.9	2490	13	US-10-027-632-111607	Sequence 111607,
31	240.4	82.9	2490	17	US-10-027-632-102144	Sequence 111607,
32	240.4	82.9	2490	17	US-10-027-632-111607	Sequence 111607,
33	240.4	82.9	10500	16	US-10-312-495-13	Sequence 13, Appl1
34	240.4	82.9	26371	13	US-10-087-192-1450	Sequence 1450, App
35	240.4	82.9	30865	17	US-10-451-867A-2	Sequence 2, Appl1
36	240.4	82.9	32249	10	US-09-764-891-5759	Sequence 5759, App
37	240.4	82.9	40000	19	US-10-741-600-18015	Sequence 18015, A
38	240.4	82.9	49620	19	US-10-852-630A-333	Sequence 233, App
39	240.4	82.9	64356	17	US-10-240-425-1100	Sequence 1100, App
40	240.4	82.9	73145	13	US-10-087-192-274	Sequence 274, App
41	240.4	82.9	146547	15	US-10-017-128-1	Sequence 1, Appl1
42	240.4	82.9	166181	18	US-10-723-860-1452	Sequence 1452, App
43	240.4	82.9	166181	18	US-10-723-860-381	Sequence 381, App
44	240.4	82.9	174448	13	US-10-087-192-148	Sequence 148, App
45	240.4	82.9	392000	15	US-10-027-983-11	Sequence 11, Appl1
46	240.4	82.9	392000	17	US-10-448-753-11	Sequence 11, Appl1
47	240.4	82.9	465237	9	US-09-933-267A-1	Sequence 1, Appl1
48	240.4	82.9	822900	17	US-10-292-798-1393	Sequence 1393, App
49	240	82.8	28933	18	US-10-712-993-6811	Sequence 6811, App
50	240	82.8	29346	17	US-10-085-117-52	Sequence 52, Appl1
51	239.4	82.6	6096	14	US-10-012-600B-132	Sequence 132, App
52	239.4	82.6	35478	18	US-10-322-281-478	Sequence 478, App
53	239.4	82.6	108316	17	US-10-292-798-1789	Sequence 1789, App
54	239.4	82.6	108317	15	US-10-017-161-2143	Sequence 2143, App
55	239	82.4	281	16	US-10-229-058B-15	Sequence 15, Appl1
56	239	82.4	665	13	US-10-027-632-152872	Sequence 152872, Sequence 152872,
57	239	82.4	665	17	US-10-027-632-152872	Sequence 152872,
58	239	82.4	913	9	US-09-764-877-3830	Sequence 3830, App
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65	238.8	82.3	2932	15	US-10-225-567A-447	Sequence 447, App
66	238.8	82.3	2932	17	US-10-305-720-1419	Sequence 1419, App
67	238.8	82.3	2932	18	US-10-755-889-595	Sequence 595, App
68	238.8	82.3	4045	10	US-09-764-891-8718	Sequence 8718, App
69	238.8	82.3	4045	10	US-09-764-891-8719	Sequence 8719, App
70	238.8	82.3	16082	19	US-10-741-600-17975	Sequence 17975, A
71	238.8	82.3	23866	19	US-10-741-600-17736	Sequence 17736, A
72	238.8	82.3	23866	19	US-10-087-192-202	Sequence 202, App
73	238.8	82.3	27204	13	US-10-087-192-1528	Sequence 1528, App
74	238.8	82.3	27204	13	US-10-087-192-1528	Sequence 2233, App
75	238.8	82.3	59588	15	US-10-017-161-2233	Sequence 1879, App
76	238.8	82.3	59588	17	US-10-292-798-1879	Sequence 61, Appl1
77	238.8	82.3	139389	17	US-10-017-128-1	Sequence 1, Appl1
78	238.8	82.3	146547	15	US-10-450-82E-86	Sequence 86, Appl1
79	238.8	82.3	160771	18	US-10-723-860-1452	Sequence 1452, App
80	238.8	82.3	160771	18	US-10-723-860-1452	Sequence 3281, App
81	238.8	82.3	166181	18	US-10-085-117-274	Sequence 274, App
82	238.8	82.3	227931	17	US-10-085-117-274	Sequence 133868,
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OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 52.8424 Seconds  
(without alignments)  
8979.909 Million cell updates/sec

Title: US-09-854-867-2  
Perfect score: 290  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:\*  
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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
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6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	249.2	85.9	282	1	US-08-133-629-8
4	245.2	84.6	36756	4	US-09-949-016-12216
5	245.2	84.6	38206	4	US-09-949-016-15527
6	245.2	84.6	63930	4	US-09-949-016-12270
7	245.2	84.6	109690	4	US-09-949-016-13525
8	243.8	84.1	601	4	US-09-949-016-36582
9	243.8	84.1	601	4	US-09-949-016-6101
10	243.8	84.1	601	4	US-09-949-016-6120
11	243.8	84.1	601	4	US-09-949-016-25489
12	243.6	84.0	601	4	US-09-949-016-73667
13	243.6	84.0	601	4	US-09-949-016-13886
14	243.6	84.0	70828	4	US-09-949-016-12122
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16	243.2	83.9	601	4	US-09-949-016-25490
17	243.2	83.9	601	4	US-09-949-016-25491
18	243.2	83.9	601	4	US-09-949-016-73668
19	243.2	83.9	601	4	US-09-949-016-73669
20	242.6	83.7	25160	4	US-09-949-016-12691
21	242.6	83.7	25162	4	US-09-949-016-13066
22	242.6	83.7	25162	4	US-09-949-016-13066
23	242	83.4	11929	4	US-09-949-016-12597
24	242	83.4	18197	4	US-09-949-016-12597
25	242	83.4	18197	4	US-09-949-016-15205
26	242	83.4	100463	4	US-09-949-016-12511
27	242	83.4	100468	4	US-09-949-016-13725

28	241.6	83.3	601	4	US-09-949-016-67217	Sequence 67217, A
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30	241	83.1	19237	4	US-09-949-016-13666	Sequence 13666, A
31	241	83.1	29927	4	US-09-949-016-11814	Sequence 11814, A
32	241	83.1	29927	4	US-09-949-016-14747	Sequence 14747, A
33	241	83.1	29927	4	US-09-949-016-17475	Sequence 17475, A
34	241	83.1	37802	4	US-09-949-016-12639	Sequence 12639, A
35	241	83.1	43550	4	US-09-949-016-12400	Sequence 12400, A
36	241	83.1	43555	4	US-09-949-016-13993	Sequence 13993, A
37	240.8	83.0	58014	4	US-09-949-016-17448	Sequence 17448, A
38	240.8	83.0	83697	4	US-09-949-016-16040	Sequence 16040, A
39	240.4	82.9	601	4	US-09-949-016-93065	Sequence 93065, A
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41	240.4	82.9	10849	4	US-09-949-016-13007	Sequence 13007, A
42	240.4	82.9	18200	4	US-09-949-016-15660	Sequence 15660, A
43	240.4	82.9	18200	4	US-09-949-016-15661	Sequence 15661, A
44	240.4	82.9	19719	4	US-09-949-016-15662	Sequence 15662, A
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46	240.4	82.9	24428	4	US-09-949-016-17262	Sequence 17262, A
47	240.4	82.9	24428	4	US-09-949-016-11752	Sequence 11752, A
48	240.4	82.9	41393	4	US-09-949-016-16012	Sequence 16012, A
49	240.4	82.9	41393	4	US-09-949-016-16492	Sequence 16492, A
50	240.4	82.9	47781	4	US-09-949-016-16493	Sequence 16493, A
51	240.4	82.9	47781	4	US-09-949-016-16494	Sequence 16494, A
52	240.4	82.9	126468	4	US-09-949-016-14418	Sequence 14418, A
53	240.4	82.9	131724	4	US-09-949-016-15893	Sequence 12893, A
54	240.4	82.9	227750	4	US-09-949-016-17175	Sequence 17175, A
55	240.4	82.9	392000	4	US-10-027-983-11	Sequence 11, Appl
56	240	82.8	601	4	US-09-949-016-93066	Sequence 93066, A
57	240	82.8	601	4	US-09-949-016-194226	Sequence 194226, A
58	239.4	82.6	678533	4	US-09-949-016-14577	Sequence 14577, A
59	239.4	82.6	678533	4	US-09-949-016-14578	Sequence 14578, A
60	238.8	82.3	601	4	US-09-949-016-59318	Sequence 59318, A
61	238.8	82.3	601	4	US-09-949-016-59319	Sequence 59319, A
62	238.8	82.3	2932	4	US-09-016-434-1419	Sequence 1419, Ap
63	238.8	82.3	2932	4	US-09-054-272-5	Sequence 5, Appl
64	238.8	82.3	18264	4	US-09-949-016-13030	Sequence 13030, A
65	238.8	82.3	46381	4	US-09-949-016-13466	Sequence 13466, A
66	238.8	82.3	62846	4	US-09-949-016-12823	Sequence 12823, A
67	238.8	82.3	92074	4	US-09-949-016-17163	Sequence 17163, A
68	238.4	82.2	601	4	US-09-949-016-14231	Sequence 14231, A
69	238.4	82.2	601	4	US-09-949-016-14232	Sequence 14232, A
70	237.8	82.0	29629	3	US-09-729-995-3	Sequence 3, Appl
71	237.8	82.0	29629	4	US-10-135-689-3	Sequence 3, Appl
72	237.8	82.0	29629	4	US-10-690-617-3	Sequence 3, Appl
73	237.8	82.0	49416	4	US-09-949-016-15334	Sequence 15234, A
74	237.6	81.9	11939	4	US-09-949-016-13232	Sequence 13232, A
75	237.2	81.8	601	4	US-09-949-016-88516	Sequence 88516, A
76	237.2	81.8	601	4	US-09-949-016-155458	Sequence 155458, A
77	237.2	81.8	601	4	US-09-949-016-175820	Sequence 175820, A
78	237.2	81.8	9208	4	US-09-949-016-15567	Sequence 15567, A
79	237.2	81.8	13248	4	US-09-949-016-12824	Sequence 12824, A
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81	237.2	81.8	14205	4	US-09-949-016-16196	Sequence 16196, A
82	237.2	81.8	14205	4	US-09-949-016-16196	Sequence 16196, A
83	237.2	81.8	17731	4	US-09-949-016-13472	Sequence 13472, A
84	237.2	81.8	17731	4	US-09-949-016-13472	Sequence 13472, A
85	237.2	81.8	22372	4	US-09-949-016-17451	Sequence 17451, A
86	237.2	81.8	23716	4	US-09-949-016-15680	Sequence 15680, A
87	237.2	81.8	24020	4	US-09-949-016-17353	Sequence 17353, A
88	237.2	81.8	33099	4	US-09-949-016-16094	Sequence 16094, A
89	237.2	81.8	34422	4	US-09-949-016-12701	Sequence 12701, A
90	237.2	81.8	34422	4	US-09-949-016-16755	Sequence 16755, A
91	237.2	81.8	36791	4	US-09-949-016-17451	Sequence 17451, A
92	237.2	81.8	41664	4	US-09-536-059-1	Sequence 1, Appl
93	237.2	81.8	53737	4	US-09-949-016-16197	Sequence 16197, A
94	237.2	81.8	57507	4	US-09-949-016-15019	Sequence 15019, A
95	237.2	81.8	63783	4	US-09-949-016-13576	Sequence 13576, A
96	237.2	81.8	94748	4	US-09-949-016-12648	Sequence 12648, A
97	237.2	81.8	94758	4	US-09-949-016-16741	Sequence 16741, A
98	237.2	81.8	96729	4	US-09-949-016-15006	Sequence 15006, A
99	237.2	81.8	100453	4	US-09-949-016-12511	Sequence 12511, A
100	237.2	81.8	100468	4	US-09-949-016-13725	Sequence 13725, A

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:44:41 ; Search time 174.09 seconds  
(without alignments)  
9861.108 Million cell updates/sec

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Perfect score: 290

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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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6	249.2	85.9	282	2	AA162346
7	248.6	85.7	291	6	AB16793
8	248.6	85.7	291	6	AB16793
9	247.4	85.3	301	10	ADH59596
10	246.8	85.1	475	4	AAK77866
11	246.8	85.1	21925	10	ADCS87602
12	243.6	84.0	825	4	AAK86384
13	243.6	84.0	1272	4	AAK73756
14	243.6	84.0	1272	4	AAK73757
15	243.6	84.0	1744	6	ABZ70301
16	243.6	84.0	60940	9	ADAO2582
17	243.6	84.0	60940	10	ADB72320
18	243.6	84.0	60940	10	ADBS5530
19	242	83.4	127145	13	ADQ80254
20	241	83.1	15577	2	AAV35616

21	241	83.1	32367	2	AAV35620	AAV35620 Human SHO
22	241	83.1	35236	11	ACN44094	ACN44094 Human gen
23	241	83.1	57502	12	ADQ97092	ADQ97092 Human can
24	241	83.1	59554	9	ADAO2696	ADAO2696 Human TK2
25	241	83.1	59554	10	ADBS72434	ADBS72434 Human TK2
26	241	83.1	59554	10	ADBS9544	ADBS9544 Human TK2
27	240.6	83.0	26184	10	ADCS87236	ADCS87236 Human GPC
28	240.4	82.9	10500	6	ABK13086	ABK13086 DNA encod
29	240.4	82.9	23130	4	AAK77045	AAK77045 Human imm
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31	240.4	82.9	30865	6	ABQ75494	ABQ75494 Human epi
32	240.4	82.9	32249	4	AA103071	AA103071 Human rep
33	240.4	82.9	32249	4	AB197407	AB197407 Human tes
34	240.4	82.9	32249	5	ABAI5833	ABAI5833 Human ner
35	240.4	82.9	73145	11	ACN44030	ACN44030 Human gen
36	240.4	82.9	110000	6	ABK90193	ABK90193
37	240.4	82.9	110000	6	ABQ87681	ABQ87681
38	240.4	82.9	110000	8	ABK37171	ABK37171
39	240.4	82.9	110000	10	ADBS1391	ADBS1391
40	240.4	82.9	110000	10	ADG70184	ADG70184
41	240.4	82.9	146547	8	ABZ80817	ABZ80817 Human pho
42	240.4	82.9	166181	12	ADQ20461	ADQ20461 Human sof
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44	240.4	82.9	174448	11	ACN43946	ACN43946 Human gen
45	240.4	82.9	238417	13	ABD32868	ABD32868 Human can
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48	240	82.8	291	4	AAK41852	AAK41852 Genomic s
49	240	82.8	291	4	AAK41901	AAK41901 Genomic s
50	240	82.8	291	4	AAK85532	AAK85532 Human imm
51	240	82.8	291	4	AAK85532	AAK85532 Human imm
52	240	82.8	291	4	AAK85482	AAK85482 Human imm
53	240	82.8	291	4	ABK92513	ABK92513 Human pro
54	239.4	82.6	6096	6	ABK92513	ABK92513 Human can
55	239.4	82.6	35478	13	ABD33376	ABD33376 Human can
56	239.4	82.6	108316	10	ADCS7336	ADCS7336 Human GPC
57	239	82.4	913	4	AA137465	AA137465 Human mus
58	239	82.4	913	12	ABX60453	ABX60453 CDNA enco
59	239	82.4	913	12	ADJ31203	ADJ31203 Human mus
60	238.8	82.3	1413	3	ADDO0684	ADDO0684 Human Hyd
61	238.8	82.3	1920	10	ADAS2630	ADAS2630 Human cod
62	238.8	82.3	2218	12	ADQ64132	ADQ64132 Novel hum
63	238.8	82.3	2227	10	ADDI1815	ADDI1815 Human pro
64	238.8	82.3	2502	13	ADBS67013	ADBS67013 Human can
65	238.8	82.3	2532	2	AAQ25388	AAQ25388 TXA2 rece
66	238.8	82.3	2532	2	AAZ32161	AAZ32161 Human thr
67	238.8	82.3	2532	2	AAZ32162	AAZ32162 Human end
68	238.8	82.3	2532	5	AA65879	AA65879 DNA encod
69	238.8	82.3	2532	8	ABK83654	ABK83654 Human CDN
70	238.8	82.3	2532	8	ABZ42829	ABZ42829 Human thr
71	238.8	82.3	2532	10	ADG32934	ADG32934 Human DNA
72	238.8	82.3	2532	12	ACAS6821	ACAS6821 Human sig
73	238.8	82.3	2932	12	ADIS6617	ADIS6617 Human pol
74	238.8	82.3	2932	12	ADQ30052	ADQ30052 Human GPC
75	238.8	82.3	2932	13	ADRI4594	ADRI4594 Human NF-
76	238.8	82.3	2932	13	ADPS6011	ADPS6011 Human PRO
77	238.8	82.3	4045	4	AA106031	AA106031 Human rep
78	238.8	82.3	4045	4	AA106030	AA106030 Human rep
79	238.8	82.3	4045	4	AB198596	AB198596 Human tes
80	238.8	82.3	4045	4	AB198595	AB198595 Human tes
81	238.8	82.3	7818	4	AAK51950	AAK51950 Human pol
82	238.8	82.3	20733	9	AAAD58742	AAAD58742 Human tra
83	238.8	82.3	24698	11	ACN43982	ACN43982 Human gen
84	238.8	82.3	27204	11	ACN44866	ACN44866 Human gen
85	238.8	82.3	32229	13	ADCS87012	ADCS87012 Human can
86	238.8	82.3	32229	11	ACN43910	ACN43910 Human gen
87	238.8	82.3	59588	10	ADCS87426	ADCS87426 Human GPC
88	238.8	82.3	139389	6	ABK84795	ABK84795 Human CDN
89	238.8	82.3	139389	9	ABD70369	ABD70369 PAC 6802
90	238.8	82.3	139389	12	ADU37148	ADU37148 Human mal
91	238.8	82.3	146547	8	ABZ80817	ABZ80817 Human pho
92	238.8	82.3	160771	6	ABO88179	ABO88179 Human ost
93	238.8	82.3	166181	12	ADQ20461	ADQ20461 Human sof

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 1330.29 Seconds

(without alignments)  
10563.118 Million cell updates/sec

Title: US-09-854-867-2

Perfect score: 290

Sequence: 1 ggcgcggcgccgctgcac.....agaccctgtcctcaaaaaa 290

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

Database:

GenBankl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290	100.0	290	12	HSU14567
2	256.4	88.4	37680	2	AL35985 Homo sapi
3	254.8	87.9	321519	2	AL714004
4	253.8	87.5	301	6	AX741027
5	253.2	87.3	110000	2	AL831785_2
6	251.4	86.7	321519	2	AL714004
7	251	86.6	283	6	AR322101
8	250	86.2	686	11	AF003745
9	250	86.2	110000	2	AL831785_4
10	249.2	85.9	282	6	I34294
11	248.6	85.7	281	6	AX335303
12	248.6	85.7	281	6	AX337621
13	248.6	85.7	281	12	HSU14573
14	248.4	85.7	83885	2	AC074301
15	248.4	85.7	195986	2	AC116933
16	248.4	85.7	223879	9	AC008735
17	248.4	85.7	235286	9	AC136285
18	247.4	85.3	301	6	AX741028
19	247.4	85.3	940	9	AY181054

20	247.4	85.3	74486	9	AC055764	AC055764 Homo sapi
21	247.4	85.3	167110	2	AC022621	AC022621 Homo sapi
22	247.4	85.3	172558	9	AC023509	AC023509 Homo sapi
23	246.8	85.1	21925	6	AX647863	AX647863 Sequence
24	246.8	85.1	37959	9	AC011551	AC011551 Homo sapi
25	246.8	85.1	69004	9	AL355145	AL355145 Homo sapi
26	246.8	85.1	69113	9	AL359860	AL359860 Homo sapi
27	246.8	85.1	148624	2	AC084815	AC084815 Homo sapi
28	246.8	85.1	165191	9	HSU140A9	AL109917 Human DNA
29	246.8	85.1	171309	9	AC012146	AC012146 Homo sapi
30	246.8	85.1	173522	2	AC073364	AC073364 Homo sapi
31	246.8	85.1	184621	2	AC104636	AC104636 Homo sapi
32	246.8	85.1	257967	2	AL365337	AL365337 Mus muscu
33	245.8	84.8	81831	2	AL365506	AL365506 Human DNA
34	245.8	84.8	115296	2	AC084815	AC084815 Homo sapi
35	245.8	84.8	128444	2	AF214634	AF214634 Homo sapi
36	245.8	84.8	168042	2	AC025931	AC025931 Homo sapi
37	245.8	84.8	181047	2	AC016765	AC016765 Homo sapi
38	245.8	84.8	198599	9	AC108448	AC108448 Homo sapi
39	245.8	84.8	221054	2	AC099882	AC099882 Homo sapi
40	245.2	84.6	56330	2	AL353694_3	Continuation (4 of
41	245.2	84.6	86560	9	AC090505	Continuation (4 of
42	245.2	84.6	120084	9	AC06205	AC06205 Homo sapi
43	245.2	84.6	128829	9	AC127002	AC127002 Homo sapi
44	245.2	84.6	129277	2	AC143642	AC143642 Macaca mu
45	245.2	84.6	141442	9	AC108471	AC108471 Homo sapi
46	245.2	84.6	146350	2	HS225L15	AL177304 Homo sapi
47	245.2	84.6	152154	2	AC136369	AC136369 Homo sapi
48	245.2	84.6	157251	2	AC131311	AC131311 Homo sapi
49	245.2	84.6	161651	9	HS233K16	AL035406 Human DNA
50	245.2	84.6	174231	9	AC021054	AC021054 Homo sapi
51	245.2	84.6	176438	2	AC126761	AC126761 Homo sapi
52	245.2	84.6	180852	2	AC126765	AC126765 Homo sapi
53	245.2	84.6	201508	2	AC026290	AC026290 Homo sapi
54	245.2	84.6	209157	9	CNS01DM4	AL136332 Human chr
55	245.2	84.6	209242	9	CNS01RGH	AL157996 Human chr
56	245.2	84.6	340000	9	HS21C100	AL163300 Homo sapi
57	244.2	84.2	2096	9	HSN43033	AL343033 Homo sapi
58	244.2	84.2	128328	9	AC005839	L35301 Homo sapien
59	244.2	84.2	146358	9	HS3D11	AC005839 Homo sapi
60	244.2	84.2	155731	9	AP001205	AP001205 Homo sapi
61	244.2	84.2	155731	9	AP001205	AC116920 Papio anu
62	244.2	84.2	174185	2	AC116930	AC116930 Homo sapi
63	243.6	84.0	8736	2	AC034158	AC034158 Homo sapi
64	243.6	84.0	25803	9	AC096510	AC096510 Homo sapi
65	243.6	84.0	40602	9	HSB140F8	Z82179 Human DNA s
66	243.6	84.0	41159	9	AC004755	AC004755 Homo sapi
67	243.6	84.0	60940	6	AX695473	AX695473 Sequence
68	243.6	84.0	72800	9	AL354757	AL354757 Human DNA
69	243.6	84.0	73463	9	AL161785	AL161785 Human DNA
70	243.6	84.0	74549	9	HSJ890015	AL049540 Human DNA
71	243.6	84.0	86156	2	AL162262	AL162262 Homo sapi
72	243.6	84.0	103694	9	AC004836	AC004836 Homo sapi
73	243.6	84.0	140489	2	AC023066	AC023066 Homo sapi
74	243.6	84.0	142391	2	AC092507	AC092507 Homo sapi
75	243.6	84.0	142527	9	AL589843	AL589843 Human DNA
76	243.6	84.0	142726	9	AC104836	AC104836 Homo sapi
77	243.6	84.0	145736	9	AL451139	AL451139 Human DNA
78	243.6	84.0	151624	2	AC072054	AL691446 Mus muscu
79	243.6	84.0	154037	2	AC072054	AC072054 Homo sapi
80	243.6	84.0	158341	2	AL713970	AL713970 Homo sapi
81	243.6	84.0	162165	2	AL162436	AL162436 Homo sapi
82	243.6	84.0	166372	2	AL162436	AL162436 Homo sapi
83	243.6	84.0	170803	2	AC016155	AC016155 Homo sapi
84	243.6	84.0	180157	9	AC015799	AC015799 Homo sapi
85	243.6	84.0	181073	2	AC011782	AC011782 Homo sapi
86	243.6	84.0	192871	9	AC040173	AC040173 Homo sapi
87	243.6	84.0	199885	2	AL353767	AL353767 Homo sapi
88	243.6	84.0	208497	2	AC090584	AC090584 Homo sapi
89	243.6	84.0	209060	9	AC010733	AC010733 Homo sapi
90	243.6	84.0	209572	9	AP003108	AP003108 Homo sapi
91	243.6	84.0	211001	9	AC018695	AC018695 Homo sapi
92	243.6	84.0	215881	2	AP001809	AP001809 Homo sapi



OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:09:22 ; Search time 649.24 Seconds

(without alignments)  
10025.556 Million cell updates/sec

Title: US-09-854-867-1

Perfect score: 171

Sequence: 1 aattctcagtaactctctctg.....ctatagaactagacagcaat 171

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	259	8	AQ106174 HS_3055_A
2	171	100.0	352	8	AQ1474179 HS_3093_A
3	171	100.0	359	8	AQ103653 HS_3093_A
4	171	100.0	371	8	AQ280392 C1TB1-E1-
5	171	100.0	373	8	AQ170834 HS_3171_A
6	171	100.0	389	8	AQ070035 HS_3027_B
7	171	100.0	389	8	AQ176209 HS_3214_B
8	171	100.0	396	8	AQ204189 HS_3107_A
9	171	100.0	398	8	AQ166366 HS_3124_B
10	171	100.0	409	8	AQ093294 HS_3018_A
11	171	100.0	414	2	AM238038 XP13H01.X
12	171	100.0	424	8	AQ090237 HS_3007_B
13	171	100.0	429	8	AQ627418 C1TB1-E1-
14	171	100.0	435	8	AQ261502 C1TB1-E1-
15	171	100.0	440	8	AQ251695 HS_3002_A
16	171	100.0	447	8	AQ183198 HS_3132_A
17	171	100.0	465	8	AQ165114 HS_3022_B
18	171	100.0	468	8	AQ147518 HS_3065_B
19	171	100.0	485	8	AQ119342 HS_3037_B
20	171	100.0	485	8	AQ253902 HS_3245_B
21	171	100.0	487	8	AQ137412 HS_3071_A
22	171	100.0	503	8	AQ260652 C1TB1-E1-
23	171	100.0	504	8	AQ124349 HS_3136_A
24	171	100.0	505	8	AQ477484 C1TB1-E1-

25	171	100.0	517	8	AQ627376 C1TB1-E1-
26	171	100.0	524	8	AQ311157 C1TB1-E1-
27	171	100.0	539	8	AQ544562 C1TB1-E1-
28	171	100.0	557	8	AQ587898 C1TB1-E1-
29	171	100.0	562	8	AQ628044 C1TB1-E1-
30	171	100.0	575	8	AQ778027 HS_3119_A
31	171	100.0	586	8	AQ625435 C1TB1-E1-
32	171	100.0	594	8	AQ626137 C1TB1-E1-
33	171	100.0	608	8	AQ428825 C1TB1-E1-
34	171	100.0	611	8	AQ261551 C1TB1-E1-
35	171	100.0	616	8	AQ394630 C1TB1-E1-
36	171	100.0	638	8	AQ545889 C1TB1-E1-
37	171	100.0	694	8	AQ263099 C1TB1-E1-
38	171	100.0	705	8	AQ624705 C1TB1-E1-
39	171	100.0	710	8	AQ895914 HS_3143_B
40	171	100.0	716	8	AQ890829 HS_3100_A
41	171	100.0	744	8	AQ897892 HS_3135_A
42	171	100.0	752	7	CF597202 AGENCOURT
43	171	100.0	770	8	AQ879157 HS_3184_B
44	171	100.0	776	8	AQ896724 HS_3144_A
45	171	100.0	823	8	AQ894357 HS_3133_A
46	171	100.0	844	8	AQ780798 HS_3104_B
47	170	99.4	436	8	AQ141211 HS_3147_B
48	170	99.4	541	8	AQ118976 HS_3002_A
49	170	99.4	562	8	AQ628431 C1TB1-E1-
50	169.4	99.1	272	8	AQ096854 HS_3040_A
51	169.4	99.1	276	8	AQ099629 HS_3056_A
52	169.4	99.1	281	8	AQ545270 C1TB1-E1-
53	169.4	99.1	373	8	AQ276733 C1TB1-E1-
54	169.4	99.1	380	8	AQ120800 HS_3076_A
55	169.4	99.1	382	8	AQ070064 HS_3027_B
56	169.4	99.1	383	8	AQ151895 HS_3104_A
57	169.4	99.1	385	8	AQ132811 HS_3078_A
58	169.4	99.1	391	8	AQ100468 HS_3061_A
59	169.4	99.1	404	8	AQ627317 C1TB1-E1-
60	169.4	99.1	405	8	AQ147619 HS_3067_B
61	169.4	99.1	417	8	AQ094572 HS_3026_B
62	169.4	99.1	420	8	AQ787454 HS_3224_B
63	169.4	99.1	438	8	AQ391364 C1TB1-E1-
64	169.4	99.1	439	8	AQ180092 HS_3204_B
65	169.4	99.1	439	8	AQ544561 C1TB1-E1-
66	169.4	99.1	464	8	AQ140268 HS_3113_A
67	169.4	99.1	473	8	AQ626094 C1TB1-E1-
68	169.4	99.1	487	8	AQ476800 C1TB1-E1-
69	169.4	99.1	490	8	AQ625170 C1TB1-E1-
70	169.4	99.1	492	8	AQ496965 HS_3044_B
71	169.4	99.1	516	8	AQ209617 HS_3236_A
72	169.4	99.1	519	8	AQ0804671 HS_3094_A
73	169.4	99.1	524	8	AQ164360 HS_3001_B
74	169.4	99.1	535	8	AQ130280 HS_3011_B
75	169.4	99.1	535	8	AQ169502 HS_3168_B
76	169.4	99.1	548	8	AQ472497 C1TB1-E1-
77	169.4	99.1	551	8	AQ475110 C1TB1-E1-
78	169.4	99.1	569	8	AQ355720 C1TB1-E1-
79	169.4	99.1	579	8	AQ628705 C1TB1-E1-
80	169.4	99.1	581	8	AQ628461 C1TB1-E1-
81	169.4	99.1	591	8	AQ390810 C1TB1-E1-
82	169.4	99.1	600	8	AQ260970 C1TB1-E1-
83	169.4	99.1	635	8	AQ626188 C1TB1-E1-
84	169.4	99.1	643	8	AQ392767 C1TB1-E1-
85	169.4	99.1	650	8	AQ393824 C1TB1-E1-
86	169.4	99.1	652	8	AQ624919 C1TB1-E1-
87	169.4	99.1	656	8	AQ626509 C1TB1-E1-
88	169.4	99.1	659	8	AQ781152 HS_3104_A
89	169.4	99.1	694	8	AQ309599 C1TB1-E1-
90	169.4	99.1	694	8	AQ392954 C1TB1-E1-
91	169.4	99.1	695	8	AQ625480 C1TB1-E1-
92	169.4	99.1	706	8	AQ425409 C1TB1-E1-
93	169.4	99.1	713	8	AQ781731 HS_3122_A
94	169.4	99.1	751	8	AQ897766 HS_3148_B
95	169.4	99.1	758	8	AQ895415 HS_3113_B
96	169.4	99.1	813	8	AQ780847 HS_3117_A
97	169.4	99.1	824	8	AQ781451 HS_3117_A

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 111.403 Seconds

(without alignments)  
9130.760 Million cell updates/sec

Title: US-09-854-867-1

Perfect score: 171  
Sequence: 1 aactccagactctctg.....ctatagaactagacagaat 171

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications NA:\*  
1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/prodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
14: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/prodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/prodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	171	10	US-09-854-867-1
2	161.4	94.4	348	9	US-09-810-935-85
3	161.4	94.4	348	9	US-09-429-755-85
4	161.4	94.4	348	9	US-09-924-400-85
5	161.4	94.4	348	15	US-10-212-679-85
6	161.4	94.4	348	17	US-10-079-137B-85
7	150.2	87.8	824	17	US-10-188-832-33
8	150.2	87.8	824	18	US-10-723-860-6919
9	150.2	87.8	824	18	US-10-723-860-8393
10	147	86.0	570	17	US-10-188-832-52
11	145.4	85.0	458	18	US-10-723-860-2854

12	145.4	85.0	458	18	US-10-723-860-4596	Sequence 4596, Ap
13	145.4	85.0	570	18	US-10-723-860-8316	Sequence 8316, Ap
14	139	81.3	464	18	US-10-723-860-4510	Sequence 4510, Ap
15	131.6	77.0	712	10	US-09-852-386-21	Sequence 21, Appl
16	131.4	76.8	293	9	US-09-810-936-86	Sequence 86, Appl
17	131.4	76.8	293	9	US-09-429-755-86	Sequence 86, Appl
18	131.4	76.8	293	9	US-09-924-400-86	Sequence 86, Appl
19	131.4	76.8	293	15	US-10-212-679-86	Sequence 86, Appl
20	131.4	76.8	293	17	US-10-079-137B-86	Sequence 86, Appl
21	121.4	71.0	674	13	US-10-027-632-228542	Sequence 228542, Ap
22	121.4	71.0	674	17	US-10-027-632-228542	Sequence 228542, Ap
23	118.8	69.5	611	13	US-10-027-632-235501	Sequence 235501, Ap
24	118.8	69.5	611	13	US-10-027-632-235502	Sequence 235502, Ap
25	118.8	69.5	611	13	US-10-027-632-235503	Sequence 235503, Ap
26	118.8	69.5	611	13	US-10-027-632-235504	Sequence 235504, Ap
27	118.8	69.5	611	13	US-10-027-632-235505	Sequence 235505, Ap
28	118.8	69.5	611	17	US-10-027-632-235501	Sequence 235501, Ap
29	118.8	69.5	611	17	US-10-027-632-235502	Sequence 235502, Ap
30	118.8	69.5	611	17	US-10-027-632-235503	Sequence 235503, Ap
31	118.8	69.5	611	17	US-10-027-632-235504	Sequence 235504, Ap
32	118.8	69.5	611	17	US-10-027-632-235505	Sequence 235505, Ap
33	117.8	68.9	784	13	US-10-027-632-325163	Sequence 325163, Ap
34	117.8	68.9	784	17	US-10-027-632-325163	Sequence 325163, Ap
35	116.2	68.0	312477	18	US-10-027-632-248758	Sequence 248758, Ap
36	114.6	67.0	689	17	US-10-027-632-248758	Sequence 248758, Ap
37	114.6	67.0	689	17	US-10-027-632-248758	Sequence 248758, Ap
38	114.6	67.0	693	16	US-10-029-386-20307	Sequence 20307, A
39	113	66.1	549	9	US-09-864-761-13107	Sequence 13107, A
40	113	66.1	589	13	US-10-027-632-235484	Sequence 235484, Ap
41	113	66.1	589	13	US-10-027-632-235485	Sequence 235485, Ap
42	113	66.1	589	17	US-10-027-632-235484	Sequence 235484, Ap
43	113	66.1	589	17	US-10-027-632-235485	Sequence 235485, Ap
44	113	66.1	604	13	US-10-027-632-235338	Sequence 235338, Ap
45	113	66.1	604	17	US-10-027-632-235338	Sequence 235338, Ap
46	112.6	65.8	624	13	US-10-027-632-203867	Sequence 203867, Ap
47	112.6	65.8	624	13	US-10-027-632-203868	Sequence 203868, Ap
48	112.6	65.8	624	17	US-10-027-632-203867	Sequence 203867, Ap
49	112.6	65.8	624	17	US-10-027-632-203868	Sequence 203868, Ap
50	111.4	65.1	534	10	US-09-918-995-4123	Sequence 4123, Ap
51	111.4	65.1	600	13	US-10-027-632-232439	Sequence 232439, Ap
52	111.4	65.1	600	13	US-10-027-632-232440	Sequence 232440, Ap
53	111.4	65.1	600	13	US-10-027-632-232441	Sequence 232441, Ap
54	111.4	65.1	600	17	US-10-027-632-232439	Sequence 232439, Ap
55	111.4	65.1	600	17	US-10-027-632-232440	Sequence 232440, Ap
56	111.4	65.1	607	17	US-10-027-632-232441	Sequence 232441, Ap
57	111.4	65.1	607	13	US-10-027-632-207009	Sequence 207009, Ap
58	111.4	65.1	607	17	US-10-027-632-207009	Sequence 207009, Ap
59	111.4	65.1	827	17	US-10-012-697-760	Sequence 760, Ap
60	111.4	65.1	1080	17	US-10-012-697-1269	Sequence 1269, Ap
61	110.8	64.8	340	9	US-09-738-973-552	Sequence 552, Ap
62	110.8	64.8	340	9	US-09-854-133-552	Sequence 552, Ap
63	110.8	64.8	340	15	US-10-144-649A-552	Sequence 552, Ap
64	110.8	64.8	445	13	US-10-027-632-183691	Sequence 183691, Ap
65	110.8	64.8	445	17	US-10-027-632-183691	Sequence 183691, Ap
66	110.2	64.4	515	13	US-10-027-632-92142	Sequence 92142, A
67	110.2	64.4	515	17	US-10-027-632-92142	Sequence 92142, A
68	109.8	64.2	586	13	US-10-027-632-185003	Sequence 185003, Ap
69	109.8	64.2	586	13	US-10-027-632-185004	Sequence 185004, Ap
70	109.8	64.2	586	13	US-10-027-632-185005	Sequence 185005, Ap
71	109.8	64.2	586	17	US-10-027-632-185003	Sequence 185003, Ap
72	109.8	64.2	586	17	US-10-027-632-185004	Sequence 185004, Ap
73	109.8	64.2	586	17	US-10-027-632-185005	Sequence 185005, Ap
74	109.8	64.2	637	13	US-10-027-632-218912	Sequence 218912, Ap
75	109.8	64.2	637	17	US-10-027-632-218912	Sequence 218912, Ap
76	109.8	64.2	1052	13	US-10-027-632-324151	Sequence 324151, Ap
77	109.8	64.2	1052	17	US-10-027-632-324151	Sequence 324151, Ap
78	109.8	64.2	2947	18	US-10-474-070-2	Sequence 2, Appl
79	109.8	64.2	2947	18	US-10-474-070-2	Sequence 2, Appl
80	108.2	63.3	405	10	US-09-918-995-1447	Sequence 3447, Ap
81	108.2	63.3	546	9	US-09-864-761-13071	Sequence 13071, A
82	108.2	63.3	1741	18	US-10-723-860-87	Sequence 87, Appl
83	108.2	63.3	1741	18	US-10-723-860-8847	Sequence 4847, Ap
84	108.2	63.3	1868	9	US-09-745-600-2	Sequence 2, Appl

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 31.1588 Seconds

(without alignments)  
8979.909 Million cell updates/sec

Title: US-09-854-867-1

Perfect score: 171  
Sequence: 1 aattccagtaactctctg.....ctatagaactagacagaat 171

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

Database:

Issued Patents NA: \*  
1: /cgn2\_6/prodata/1/ina/5A COMB.seq: \*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq: \*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq: \*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/PC/TUS COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	171	4	US-09-573-080A-1
2	161.4	94.4	348	3	US-08-991-789A-85
3	161.4	94.4	348	3	US-09-062-451-85
4	161.4	94.4	348	3	US-09-598-326-85
5	161.4	94.4	348	4	US-09-289-198-85
6	161.4	94.4	348	4	US-09-429-755-85
7	161.4	94.4	348	4	US-09-699-295-85
8	131.4	76.8	293	3	US-08-991-789A-86
9	131.4	76.8	293	3	US-09-062-451-86
10	131.4	76.8	293	3	US-09-598-326-86
11	131.4	76.8	293	4	US-09-289-198-86
12	131.4	76.8	293	4	US-09-429-755-86
13	131.4	76.8	293	4	US-09-699-295-86
14	112.6	65.8	351	4	US-09-513-999C-34318
15	111.4	65.1	360	4	US-09-513-999C-20597
16	110.8	64.8	360	4	US-09-513-999C-32817
17	108.2	63.3	1868	4	US-09-554-133-552
18	108.2	63.3	1868	4	US-09-745-600-2
19	107.6	62.9	171	1	US-07-858-124-20
20	106.6	62.3	109038	4	US-09-949-016-12199
21	104.6	60.9	419	4	US-09-513-999C-32817
22	101.8	59.5	339	3	US-09-554-028-4
23	101.8	59.5	339	3	US-09-554-028-5
24	101.8	59.5	339	3	US-09-745-600-4
25	101.8	59.5	339	4	US-09-745-600-5
26	101.2	59.2	171	1	US-07-858-124-22
27	101	59.1	161	1	US-07-858-124-16

28	101	59.1	1044	3	US-08-695-191-2	Sequence 2, Appl
29	101	59.1	1044	3	US-08-682-080-2	Sequence 2, Appl
30	101	59.1	1044	3	US-09-096-648-2	Sequence 2, Appl
31	99	57.9	197	1	US-07-858-124-18	Sequence 18, Appl
32	97.4	57.0	253	4	US-09-513-999C-22522	Sequence 22522, A
33	97.4	57.0	197	1	US-07-858-124-17	Sequence 17, Appl
34	93.4	54.6	338	3	US-09-254-028-7	Sequence 7, Appl
35	93.4	54.6	338	3	US-09-745-600-7	Sequence 7, Appl
36	92.8	54.3	601	4	US-09-949-016-161507	Sequence 161507, A
37	92.8	54.3	240157	4	US-09-513-999C-22100	Sequence 22100, A
38	91.6	53.6	507	4	US-09-513-999C-16264	Sequence 16264, A
39	91.4	53.5	338	3	US-09-254-028-3	Sequence 3, Appl
40	91.4	53.5	338	3	US-09-745-600-3	Sequence 3, Appl
41	87.6	51.2	340	3	US-09-254-028-6	Sequence 6, Appl
42	87.6	51.2	340	3	US-09-745-600-6	Sequence 6, Appl
43	82.6	48.3	343	3	US-09-643-597-142	Sequence 142, App
44	82.6	48.3	343	4	US-09-480-884A-142	Sequence 142, App
45	82.6	48.3	343	4	US-09-542-615A-142	Sequence 142, App
46	82.6	48.3	343	4	US-09-606-421B-142	Sequence 142, App
47	82.6	48.3	343	4	US-09-221-107-142	Sequence 142, App
48	82.6	48.3	343	4	US-09-466-396A-142	Sequence 142, App
49	82.6	48.3	343	4	US-09-476-496A-142	Sequence 142, App
50	82.6	48.3	343	4	US-09-630-940B-142	Sequence 142, App
51	82.6	48.3	343	4	US-09-285-479-142	Sequence 142, App
52	81.6	47.7	130	1	US-07-938-084-4	Sequence 4, Appl
53	79.2	46.3	176	4	US-09-513-999C-14727	Sequence 14727, A
54	76.8	44.9	283	4	US-09-513-999C-35464	Sequence 35464, A
55	72.8	42.6	131	1	US-07-938-084-5	Sequence 5, Appl
56	71.6	41.9	182	4	US-09-513-999C-20755	Sequence 20755, A
57	67.4	39.4	858	3	US-09-333-521-2	Sequence 2, Appl
58	67.4	39.4	858	3	US-09-899-863A-2	Sequence 2, Appl
59	65.6	38.4	130	1	US-07-938-084-6	Sequence 6, Appl
60	64.6	37.8	171	1	US-07-858-124-19	Sequence 19, Appl
61	64.2	37.5	5829	3	US-09-439-311-473	Sequence 473, App
62	64.2	37.5	5829	3	US-09-636-215-473	Sequence 473, App
63	64.2	37.5	5829	4	US-09-685-166A-473	Sequence 473, App
64	64.2	37.5	5829	4	US-09-679-426-473	Sequence 473, App
65	64.2	37.5	5829	4	US-09-759-143-473	Sequence 473, App
66	64.2	37.5	5829	4	US-09-651-236-473	Sequence 473, App
67	62.6	36.6	100	1	US-07-938-084-11	Sequence 11, Appl
68	62.6	36.6	474	4	US-09-621-976-16748	Sequence 16748, A
69	57.2	33.5	146	4	US-09-513-999C-16140	Sequence 16140, A
70	54.8	32.0	174	1	US-07-858-124-21	Sequence 21, Appl
71	48.2	28.2	80	1	US-07-938-084-10	Sequence 10, Appl
72	48	28.1	192	1	US-08-153-051B-21	Sequence 21, Appl
73	48	28.1	192	1	US-08-060-955C-37	Sequence 37, Appl
74	48	28.1	192	2	US-08-151-477A-21	Sequence 21, Appl
75	48	28.1	192	3	US-08-819-867-51	Sequence 51, Appl
76	48	28.1	192	3	US-08-464-011B-37	Sequence 37, Appl
77	48	28.1	192	4	US-09-378-535-51	Sequence 51, Appl
78	38.4	22.5	80	3	US-09-308-759A-18	Sequence 18, Appl
79	37.2	21.8	60	1	US-07-938-084-9	Sequence 9, Appl
80	37.2	21.8	61	4	US-09-513-999C-27263	Sequence 27263, A
81	35.6	20.8	858	3	US-09-333-521-2	Sequence 2, Appl
82	35.6	20.8	858	4	US-09-899-863A-2	Sequence 2, Appl
83	35.4	20.7	190078	4	US-09-949-016-12707	Sequence 12707, A
84	35.4	20.7	190078	4	US-09-949-016-17026	Sequence 17026, A
85	35	20.5	252	4	US-09-513-999C-27943	Sequence 27943, A
86	34.4	20.1	177293	4	US-09-949-016-16513	Sequence 16513, A
87	33.6	19.6	50	2	US-08-843-468-5	Sequence 5, Appl
88	33.6	19.6	85850	4	US-09-949-016-1424	Sequence 1424, A
89	33.4	19.5	601	4	US-09-949-016-53880	Sequence 53880, A
90	33.4	19.5	75176	4	US-09-949-016-13300	Sequence 13300, A
91	33	19.3	231293	4	US-09-949-016-16110	Sequence 16110, A
92	33	19.3	266293	4	US-09-949-016-11934	Sequence 11934, A
93	32.6	18.7	601	4	US-09-949-016-156497	Sequence 156497, A
94	32	18.7	601	4	US-09-949-016-184461	Sequence 184461, A
95	30.6	17.9	601	4	US-09-949-016-184464	Sequence 184464, A
96	30.6	17.9	601	4	US-09-949-016-184465	Sequence 184465, A
97	30.2	17.7	5064	3	US-08-938-107A-8	Sequence 8, Appl
98	29.8	17.4	826	4	US-09-919-112-99	Sequence 99, Appl
99	29.8	17.4	826	4	US-09-976-594-811	Sequence 811, App
100	29.8	17.4	4821	3	US-08-913-374-1	Sequence 1, Appl

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:44:41 ; Search time 102.653 Seconds

(without alignments)  
9861.108 Million cell updates/sec

Title: US-09-854-867-1

Perfect score: 171

Sequence: 1 aattctcgtactctctg.....ctatagaactagacagat 171

Scoring table:

IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

1: N\_Geneseq\_16Dec04:\*  
2: Geneseq19808:\*  
3: Geneseq19908:\*  
4: Geneseq20008:\*  
5: Geneseq20018:\*  
6: Geneseq20028:\*  
7: Geneseq20038:\*  
8: Geneseq20048:\*  
9: Geneseq20058:\*  
10: Geneseq20068:\*  
11: Geneseq20078:\*  
12: Geneseq20088:\*  
13: Geneseq20098:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	171	100.0	171	7	AD830968 Human, gen
2	170.2	99.5	265	10	ACD93531 Human col
3	169	98.8	221	10	ACD93531 Human col
4	161.4	94.4	348	2	AA83284 Breast ca
5	161.4	94.4	348	2	AA83284 Breast ca
6	161.4	94.4	348	2	AA83284 Breast ca
7	161.4	94.4	348	2	AA83284 Breast ca
8	161.4	94.4	348	2	AA83284 Breast ca
9	161.4	94.4	348	2	AA83284 Breast ca
10	161.4	94.4	348	2	AA83284 Breast ca
11	150.2	87.8	824	8	ACC50969 Human bla
12	150.2	87.8	824	8	ACC50969 Human bla
13	150.2	87.8	824	8	ACC50969 Human bla
14	147	86.0	570	8	ACC50979 Human bla
15	145.4	85.0	458	12	ADQ20034 Human sof
16	145.4	85.0	458	12	ADQ20034 Human sof
17	145.4	85.0	458	12	ADQ20034 Human sof
18	142.2	83.2	570	12	ADQ25496 Human sof
19	139	81.3	464	12	ADQ25496 Human sof
20	131.6	77.0	712	6	ABK27490 DNA encod

21	131.4	76.8	293	2	AA83285 Breast ca
22	131.4	76.8	293	2	AA83285 Breast ca
23	131.4	76.8	293	2	AA83285 Breast ca
24	131.4	76.8	293	2	AA83285 Breast ca
25	131.4	76.8	293	2	AA83285 Breast ca
26	131.4	76.8	293	2	AA83285 Breast ca
27	131.4	76.8	293	2	AA83285 Breast ca
28	115.6	67.0	312477	12	ADP69744 Human ROC
29	115.6	67.0	312477	12	ADP69744 Human ROC
30	113.2	66.2	693	12	ACH87112 Human gen
31	113.2	66.2	693	12	ACH87112 Human gen
32	113	66.1	257	13	ADR37541 Human alp
33	113	66.1	257	13	ADR37541 Human alp
34	113	66.1	257	13	ADR37541 Human alp
35	113	66.1	257	13	ADR37541 Human alp
36	112.6	65.8	351	3	AA83043 Human sec
37	111.4	65.1	360	3	AA83043 Human sec
38	111.4	65.1	360	3	AA83043 Human sec
39	111.4	65.1	360	3	AA83043 Human sec
40	111.4	65.1	360	3	AA83043 Human sec
41	111.4	65.1	360	3	AA83043 Human sec
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44	110.8	64.8	340	10	ADP63085 Human jun
45	110.8	64.8	340	10	ADP63085 Human jun
46	110.8	64.8	340	10	ADP63085 Human jun
47	110.4	64.2	2026	5	AA171672 Human myo
48	109.8	63.6	2847	10	AA49908 Human alp
49	108.8	63.6	2950	10	AA49908 Human alp
50	108.2	63.3	405	9	ACH16235 Human adu
51	108.2	63.3	405	9	ACH16235 Human adu
52	108.2	63.3	405	9	ACH16235 Human adu
53	108.2	63.3	405	9	ACH16235 Human adu
54	108.2	63.3	405	9	ACH16235 Human adu
55	108.2	63.3	405	9	ACH16235 Human adu
56	108.2	63.3	405	9	ACH16235 Human adu
57	108.2	63.3	405	9	ACH16235 Human adu
58	108.2	63.3	405	9	ACH16235 Human adu
59	106.6	62.3	523	12	ACH73386 Human pro
60	106.6	62.3	523	12	ACH73386 Human pro
61	106.6	62.3	523	12	ACH73386 Human pro
62	106.6	62.3	523	12	ACH73386 Human pro
63	106.6	62.3	523	12	ACH73386 Human pro
64	106.6	62.3	523	12	ACH73386 Human pro
65	105.2	61.5	357	2	AA61362 Human bra
66	105.2	61.5	357	2	AA61362 Human bra
67	105.2	61.5	357	2	AA61362 Human bra
68	104.2	60.9	419	3	AA28742 Human bra
69	104.2	60.9	419	3	AA28742 Human bra
70	103.6	60.6	334	4	AAK76728 Human bra
71	103.4	60.5	541	12	ACH71431 Human gen
72	103.4	60.5	541	12	ACH71431 Human gen
73	103.4	60.5	541	12	ACH71431 Human gen
74	103.4	60.5	541	12	ACH71431 Human gen
75	102	59.6	306	4	AA830912 Human cdn
76	101.8	59.5	339	2	AAV24224 Fragment
77	101.8	59.5	339	2	AAV24224 Fragment
78	101.8	59.5	339	2	AAV24224 Fragment
79	101.8	59.5	339	2	AAV24224 Fragment
80	101	59.1	1044	8	ADA14732 Human hex
81	101	59.1	1044	8	ADA14732 Human hex
82	100.4	58.7	334	4	AAK76727 Human bra
83	100.4	58.7	334	4	AAK76727 Human bra
84	100.4	58.7	334	4	AAK76727 Human bra
85	100.4	58.7	334	4	AAK76727 Human bra
86	100	58.5	398	4	AAK76733 Human imm
87	99.8	58.4	1044	8	ABX10710 DNA fragm
88	99.2	58.0	510	12	ACH73118 Human gen
89	99.2	58.0	510	12	ACH73118 Human gen
90	99	57.9	263	3	AA830027 PCR produ
91	98.8	57.7	367	5	ABV58247 Human pro
92	98.6	57.7	367	5	ABV58247 Human pro
93	97.8	57.2	336	10	ADK11642 Breast ca

## OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 784.412 Seconds

(without alignments)  
10563.118 Million cell updates/sec

Title: US-09-854-867-1

Perfect score: 171

Sequence: 1 aatctcagaactctctg.....ctatagaactagacagaat 171

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

## Database :

1: gb\_ba:\*  
2: gb\_hhg:\*  
3: gb\_in:\*  
4: gb\_in:\*  
5: gb\_cv:\*  
6: gb\_cv:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	171	100.0	340 9 HUMSCNT	K00901 Human cent
2	171	100.0	340 9 HUMSCNT	M20434 Human alph
3	171	100.0	342 9 HUMSAT1	J00305 human tand
4	171	100.0	110000 2 AL831785	Continuation (8 of
5	171	100.0	165291 2 AC114775	AC114775 Homo sapi
6	171	100.0	166105 2 AC104603	AC104603 Drosophi
7	169.4	99.1	171 9 HSAR1071	X13630 Human alph
8	169.4	99.1	171 9 HSAR1261	X13632 Human alph
9	169.4	99.1	340 9 HSPS3C	X60711 Human clone
10	169.4	99.1	685 9 HSA295044	AJ295044 Homo sapi
11	169.4	99.1	93161 2 AC135046	AC135046 Homo sapi
12	169.4	99.1	321519 2 AL714004	AL714004 Homo sapi
13	168.4	98.5	280 9 HS286CR	Z55240 H. sapiens C
14	167.8	98.1	338 9 S49993	S49993 [R-DNA, alp
15	167.8	98.1	93161 2 AC135046	AC135046 Homo sapi
16	166.2	97.2	171 9 HSAR31	AC104603 Drosophi
17	166.2	97.2	344 9 HUMSCNT	X13634 Human alph
18	166.2	97.2	118550 2 BX322633	M18124 Human alph
19	166.2	97.2	118550 2 BX322633	BX322633 Homo sapi

22	166.2	97.2	163824 2	BX284928	BX284928 Homo sapi
23	165.8	97.0	171 9	HSREPI	V00579 Human repet
24	165.8	97.0	277 9	HS90G9F	Z63828 H. sapiens C
25	165.2	96.6	185887 2	AC133553	AC133553 Homo sapi
26	164.6	96.3	171 9	HSAR1341	X13636 Human alph
27	164.6	96.3	340 9	HUMSCNTN	M20435 Human alph
28	164.6	96.3	344 9	HUMSCNTI	M18123 Human alph
29	164.6	96.3	171474 2	AC135053	AC135053 Homo sapi
30	163	95.3	171 9	HSAR51	X13642 Human alph
31	163	95.3	171 9	HSAR51	X13645 Human alph
32	163	95.3	171 9	HSAR61	X13648 Human alph
33	163	95.3	346 9	HSAR25042	AJ295042 Homo sapi
34	163	95.3	302746 2	AC140814	AC140814 Homo sapi
35	161.4	94.4	171 9	HSAR1231	X13647 Human alph
36	161.4	94.4	171 9	HSAR911	X13647 Human alph
37	161.4	94.4	302 9	HS5CAF	Z65792 H. sapiens C
38	161.4	94.4	344 9	HUMSCNTH	M18122 Human alph
39	161.4	94.4	344 9	HUMSCNTK	M21871 Human alph
40	161.4	94.4	348 6	AR147916	AR147916 Sequence
41	161.4	94.4	348 6	AR219640	AR219640 Sequence
42	161.4	94.4	348 6	AR350738	AR350738 Sequence
43	161.4	94.4	348 6	AR433114	AR433114 Sequence
44	161.4	94.4	348 6	AX316748	AX316748 Sequence
45	161.4	94.4	348 6	BD084231	BD084231 Compositi
46	161.4	94.4	680 9	HUMSATD	M58446 Human alph
47	161.4	94.4	138800 2	AC140816	AC140816 Homo sapi
48	161.4	94.4	138829 2	AL391668	AL391668 Homo sapi
49	161.4	94.4	198829 2	AL391668	AL391668 Homo sapi
50	159.8	93.5	171 9	HSAR21	X13640 Human alph
51	159.8	93.5	171 9	HSAR81	X13649 Human alph
52	159.8	93.5	644 9	AJ717298	AJ717298 Homo sapi
53	159.8	93.5	302746 2	AC140814	AC140814 Homo sapi
54	159.4	93.2	275 9	HS12B11F	Z56579 H. sapiens C
55	158.6	92.7	159530 2	AC133922	AC133922 Homo sapi
56	158.2	92.5	171 9	HSAR1151	X13644 Human alph
57	158.2	92.5	171 9	HUMSATAL	M27772 Human alph
58	158.2	92.5	318 9	HS36D10R	Z60841 H. sapiens C
59	158.2	92.5	344 9	HUMSCNTG	M18121 Human alph
60	156.8	91.7	279 9	HS30G4R	Z58181 H. sapiens C
61	156.6	91.6	43705 9	AC010517	AC010517 Homo sapi
62	156.2	91.3	313 9	HS37A8R	Z55373 H. sapiens C
63	155	90.6	166111 2	AC073442	AC073442 Homo sapi
64	154.6	89.4	171 9	HS18H3F	Z57696 H. sapiens C
65	152.4	89.1	171 9	HUMSATAP	M27778 Human alph
66	148.6	86.9	3906 9	HSATITIA	X67031 H. sapiens D
67	148.6	86.9	167060 2	AC141296	AC141296 Homo sapi
68	148.6	86.9	174688 9	AC026131	AC026131 Homo sapi
69	148.6	86.9	185972 2	AC069355	AC069355 Homo sapi
70	148.6	86.9	191752 2	BX322613	BX322613 Human DNA
71	147	85.0	168763 9	AC146133	AC146133 Pan trogl
72	146.2	85.5	341 9	HUMSCNTT	M20441 Human alph
73	146.2	85.5	1049 9	HUMSATAC	M26920 Human alph
74	145.4	85.0	110000 2	AC148612_1	Continuation (2 of
75	145.4	85.0	110000 2	AC148612_2	Continuation (3 of
76	144.4	84.4	340 9	HUMSCNTU	M20442 Human alph
77	144	84.2	336 9	HS26E1R	Z58018 H. sapiens C
78	143.8	84.1	171 9	HUMSATAK	M27771 Human alph
79	143.8	84.1	334 9	S49988	S49988 [R-DNA, alp
80	143.8	84.1	3529 9	AC123578	AC123578 Homo sapi
81	143.8	84.1	69462 2	AC073925	AC073925 Homo sapi
82	143.8	84.1	187282 9	AC019063	AC019063 Homo sapi
83	142.4	83.3	172 9	HUMSATAG	M27777 Human alph
84	142.4	83.2	33836 9	AC142529	AC142529 Homo sapi
85	142.2	83.2	110000 2	AL811785_2	Continuation (3 of
86	142.2	83.2	153616 2	AC136945	AC136945 Homo sapi
87	142.2	83.2	158766 2	AC137793	AC137793 Homo sapi
88	142	83.0	308 9	HS43DSF	Z61072 H. sapiens C
89	141	82.5	166 9	HUMARDNA	M28426 Human alph
90	140.8	82.3	336 9	HS7D3R	Z66184 H. sapiens C
91	140.6	82.2	343 9	HUMSCNTF	M18124 Human alph
92	140.6	82.2	680 9	HUMSATAT7C	M16101 Human tetra